

Clone	Sequence
Desigņ	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
R40-3-40B2-IR	IRDMHYVWVQDRDRYINGVRQWYISDRYNPGSAFYRWFID
/Ra0-4-40B12-IR	RMGLQALAHYRKSAGPIFLSSGSVIKGSEGDPFYAWFRLQ
R40-4-40G11-1R	MPVSLFRRVWDYRDGEHETLESHYVVPQAALDRLFYSWFS

Ratios over Background
E-Tag IGFsR IR
-- -- -- -- 40.3 9.0 2.0
60.4 12.9 2.0
52.6 37.5 2.0

Comparisons IGFR/IR IR/IGFR

2.0

Figure 1A



R40-X-R35-IGFR R40-3-D5-IGFR R40-3-A6-IGFR Sequence SGCCRLLGLRWMFIVIVGWSGALVCQSAASAAGFYDWFV YRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDWFV PLYGGGIHLYYPGTMGYVPGFPRQVKVLGDADKNFYDWFM

Clone

Девідп

Ratios over Background E-Tag IGFsR IR Comparisons
IGFR/IR IR/IGFR



			R20 }-4-A8-IR IGGSFVEFYGWFNDQV	R20β-4-F4-IR GVGTLTMSSDAFYTWFV	R20 3-4-E2-IR SRDQTNFTFNSAGFYGWFER	R20β-4-B8-IR WSALLSVMDTGFYAWFDDAV	R20β-4-H8-IR RDKPTDQEEQNWSFYEWFRH	R20 }-4-H9-IR IGGQGQHQDGNFYDWFVEALA	R20 }-4-G8-IR RMFYEWFWSQMGAGPTEGSA	R20β-4-G11-IR FYGWFSRQLSLTPRDDWGLP	R20 -4-H6-IR NSSGQQVVGLTFYSWFASQV	R20β-4-G3-IR RGGGTFYEWFESALRKHGAG	R20β-4-E7-2-IR LGTSAGQGVGHRAFYQWFQS	R20 }-4-E7-IR GHSWALVRHVDRLFYEWFDL	R20 }-4-C8-IR LPAGGA?GFA?RGFYEWFES	R20 }-4-D10-2-IR RIGGGWARSEGFYEWFVREL	R20 }-4-H3-IR HEAFYDWFSALVDGGYELMG	R20  -4-B12-IR GAFYRWFHEALVGSERVPDV	R20α-3-20D1-IR VLQARHGCDSVSDCFYEWFA	R200-3-20H1-IR RVAGAISAPGLVSNKQDGLFYSWFRE	R20u-3-20f1-IR VFWNCRSQQLDFYEWFEQAA	R20α-3-20D3-IR IGGQGQHQDGNFYDWFVEALA	Design XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	Clone Sequence
44.8	17.3	17 7	43.3	15.3	16.3	44.0	47.9	43.1	41.2	39.4	14.8	38.6	45.0	45.0	44.9	21.5	13.9	41.9	50.8	45.6	49.0	46.3	;	Ratios ove E-Tag
36.2	20.0	26.8	36.0	5.9	13.9	40.1	43.7	8.8	15.1	7.5	7.6	7.5	18.8	18.8	31.1	7.3	5.8	2.9	37.5	35.3	26.0	36.2	;	ver Background IGFsR II
						œ	9	2.	ω ·	1.5	2.0	2.0	5.5	. 5. 9	9.6	2.9	2.4	5.7	3.0	ω . ω	2.8	7.0	;	und IR
5.6	1 £	، ۵	6.0	1.0	2.4	.4	·w	0	4.	w	_	_	•											
5.6 6.5	٠.	4 2 6 2	6.0 6.0	1.0 5.9	2.4 5.8	.4 4.8	.4	.4		ω	ω	w	w	ω	3.2	2.5	2.4	•	12.5	10.7	9.3	5.2	;	Comparisons IGFR/IR IR/IGFR

Figure 1C



R20-4-G12-IGFR R20-4-D10-IGFR	R20-4-F8-IGFR	R20-4-B9-IGFR	<b>Design</b>	Clone
PFYQWFLDQSVGGSRGGGLR AVAPLSVRGRDSGFYSWFSS	DIGSDGHGRRWDSFYRWFEM	DPERMOSDVGFYEWFRAAVG	XXXXXXXXXXXXXXXXXX	Sequence

Ratios ov	Ratios over Background	uno.	Comparisons	risons	
Ę-Tag	IGFsR	₹	IGFR/IR IR/IGFR	IR/IGFR	
;	1	:	;	:	
40.1	16.6	;	1	;	
39.2	13.9	!		1	
36.7	9.0	1	:	;	
40.2	4.1	!	1	•	



MASWQSRTPDNFYDWFVRELS	A6S-3-E4-IR
VRVVLNQSGRNFYDWFVIQLE	A6S-2-C5-IR
DWDKLGSLSENFYDWFVDQLA	A6S-3-F1-IR
DRQSIGSVHGDFYDWFVSALG	A6S-2-C2-IR
TLEREGEFSGNFYDWFVEQLH	A6S-4-G6-IR
ASHQRGGSSDNFYDWFVAQMR	A6S-3-E7-IR
PWMLSVGIQDNFYDWFVGLDS	A6S-1-B7-IR
PEARRTVVHSNFYDWFVAQLS	A6S-3-E5-IR
LDGTKACQRVNFYDWFVCQTE	A6S-3-F3-IR
DQQRSACDGTNFYDWFVCQLS	A6S-2-C11-IR
LMQSLGSGSTNFYDWFVQQMV	A6S-2-C3-IR
RQPSQPPHGSNFYDWFVEAIN	A6S-4-H2-IR
GQEYFDQMGLNFYDWFVRELD	A6S-4-G7-IR
LAQFAGSRNQNFYDWFVEQLG	A6S-4-H10-IR
SREAVOKRNANFYDWFVQQLS	A6S-2-C4-IR
VGTGRARLDRNFYDWFVGQYS	A6S-2-C9-IR
MSEPAVGVNGNFYDWFVAQLF	A6S-1-A1-IR
GQAQLSIRDVNFYDWFVQQLV	A6S-3-E11-IR
RQSEFSTLNSNFYDWFVRELE	A6S-4-H8-IR
RLASASVPGQNFYDWFVDQLL	A6S-4-G3-IR
PHGHRGFAQSNFYDWFVTQEE	A6S-1-A4-IR
TDRKSVQEPRNFYDWFVWAAR	A6S-1-B2-IR
AIQMNGNLAFNFYDWFVRELT	A6S-2-D5-IR
AMHVVAQGGPNFYDWFVRELR	A6S-3-E10-IR
MHRMQHDGTSNFYDWFVLQWA	A6S-2-C8-IR
HHTQGLQVQRNFYDWFVNELR	A6S-1-A7-IR
RMYFSTGAPQNFYDWFVQEWD	A6S-2-C1-IR
GRVDWLQRNANFYDWFVAELG	A6S-3-E12-IR
XXXXXXXXXNFYDWFVXXXX	Design
Sequence	Clone

Ratios ov E-Tag	Ratios over Background E-Tag IGFsR II	R	Compai IGFIVIR	Comparisons FR/IR IR/ICFR
ı	•	:	:	4
26.2	1.3	8.0	0.2	6.2
41.2	1.3		•	5.4
47.2	2.3			4.8
44.9	1.5	5.5	0.3	3.7
46.9	-		•	3.1
31.9				3.1
31.6	-		•	2.9
43.3	-			2.6
_	-			2.2
$\mathbf{L}$	-			
9	_		•	
36.9	_			
w	_			•
Ā	_	•		
39.2	4.4		0.6	1.6
9			•	•
ū	_		•	
_	_	•	•	
0	_		0.7	•
37.1	-		0.7	•
31.6			0.7	•
49.2	-		0.7	1.4
37.2		•	0.8	1.3
16.8			0.8	1.3
29.7		•	0.8	1.3
9	2.3	•	0.8	1.3
42.9	6.1	•	0.9	1.1
0	2.1	•	0.9	1.1

Figure 1E



SLGRNDRPDENFYDWFVSQVQ RVMATANAPMNFYDWFVVQLQ	A6S-3-F9-IR A6S-3-F2-IR
VDRAGPAGSDNFYDWFVAQLD	6-4-G10-
SGPVVQTQNGNFYDWFVHQLR	A6S-2-D7-IR
GKLVASTLDDNFYDWFVROLS	-G12
EDRIGNGESTNEYDWFVROLA	A6S-4-G4-IR
RLDVAGHRGGNFYDWFVKQLH	<u>ئۇ</u> 1
MEGPPAGGPLNFYDWFVAQVD	A6S-3-F6-IR
NLKSSATVGGNFYDWFVEQL	A6S-4-H1-IR
ERFALEVQGSNFYDWFVRQVI	A6S-3-F5-IR
GPGRHDSSRGNFYDWFVEQLA	A6S-4-G9-IR
GVSRGSGDPNFYDWFVMQLR	A6S-3-F4-IR
PQPRSASTPLNFYDWFVQATG	A6S-2-D10-IR
VCDVSTGGGTNFYDWFVCQVG	A6S-4-H6-IR
EAIMREEGQANFYDWFVRQLE	A6S-4-G8-IR
QDTFLTAREGNFYDWFIRALE	A6S-2-D2-IR
HRQQDVVRQGNFYDWFVQAL	A6S-4-G11-IR
GSSLGRSGPGNFYDWFVDQLE	A6S-3-F10-IR
VGEHRQMSVGNFYDWFVMQIA	A6S-2-D8-IR
GVSIQAGYKTNFYDWFVEAVR	A6S-3-F7-IR
GADDIRSLNTNFYDWFVNQLS	A6S-4-H3-IR
<b>DVGMGRVKETNFYDWFVRQLI</b>	A6S-1-A12-IR
PQSLTEVRTGNFYDWFVVQLH	A6\$-3-E8-IR
ESLTGSRPDRNFYDWFVQQTS	A6S-2-D3-IR
TPRSQVRSDHNFYDWFVYQLA	A6S-4-H12-IR
VRGNDSVLRANFYDWFVDQLS	A6\$-3-E1-IR
TTCHPRGEDCNFYDWFVLQLR	A6S-3-E9-IR
XXXXXXXXXXNFYDWFVXXXX	D sign
Sequence	Clone

	Ratios ove	ios over Backgroun ag IGFsR	und IR	Compar IGFR/IR	risons IR/IGFR
	:	:	:	1	:
	36.6	9.0	8.9	1.0	1.0
	36.7	6.8	•	1.0	1.0
	46.3	6.1	5.8	1.1	1.0
	37.0	5.3	5.1	1.0	1.0
	42.7	5.2	5.1	1.0	1.0
	39.7	2.1	2.1	1.0	1.0
	18.6	3.1		1.1	0.9
	46.2	2.3	2.1	1.1	. 0.9
	31.2	2.0		1.2	0.9
	39.0	5.9	4.5	1.3	0.8
	44.8	4.3	٠ 	1.3	0.8
	33.5	3.6	2.7	1.3	0. d
	11.1	2.5	1.9	1.3	0.8
-	22.4	2.4	1.9	1.3	0.8
	41.3	2.1	1.7	1.2	0.8
	37.0	13.5	9.9	1.4	0.7
	36.2	11.8	7.8	1.5	0.7
	48.1	7.2	4.8	1.5	0.7
	18.3	3.6	2.6	1.4	0.7
	18.7	2.9	1.9	1.5	0.7
	33.8	2.0	1.4	1.4	0.7
	46.7	19.2	12.1	1.6	0.6
	36.9	18.2	10.7	1.7	0.6
	32.8	12.8	7.9	1.6	0.6
	33.2	12.0	7.1	1.7	0.6
	33.9	10.8	6.8	1.6	0.6
	44.3	9.6	5.7	1.7	0.6
	23.2	4.3	2.5	1.7	0.6

Figure 1E (Con't)



Tone	Sequence
)esign	XXXXXXXXXXNFYDWFVXXXX
6S-4-G1-IR	NGVERAGTGDNFYDWFVAQLH
6S-1-A3-IR	PFAGKGDKTGNFYDWFVSLTG
6S-3-F12-IR	GMPQEYMDQVNFYDWFVAQVD
6S-4-G2-IR	MGTPAVGDGANFYDWFVRQLG
6S-1-B1-IR	SKCKAWYGANNFYDWFVWQVD
6S-2-D11-IR	<b>EAASLGSQDRNFYDWFVRQVV</b>
6S-2-D1-IR	VERSASSQDGNFYDWFVVQIR
6S-3-E2-IR	TSEVQRRSQDNFYDWFVAQVA

Ratios ov	Ratios over Background	en d	Comparisons	risons TR/ICER	
		: ;		1	
36.2	31.8	15.7	2.0	0.5	
39.9	12.6	6.0	2.1	0.5	
41.4	7.4	4.0	1.9	0.5	
26.7	7.0	J.5	2.0	0.5	
30.6	3.7	1.9	1.9	0.5	
48.4	37.4	13.5	2.8	0.4	
37.8	30.6	12.0	2.6	0.4	
33.1	24.7	9.8	2.5	0.4	



30	17	18	19	21	22	22	25	20	25	37	18	19	23	24	42	20	20	24	25	36	40	21	26	26	35	36	27		E-Tag	Ratios ov
23	24	24	24	24	24	24	24	25	25	25	26	26	26	26	27	28	28	28	28	28	28	29	30	30	30	30	32	1	E-Tag IGFsR II	er Backgro
;	1	1	1	;	1	1	1	1	1	1	1	1	1	1	!	1	1	1	1	:	•	1	!	1	;	1	1	•	≅	bund
i I	1	1	1	:	!	!	!	!	,	1 1		:	1	1	!	1	1		1	1	1	1	1	!	1	!	1	;	IGFR/IR IR/IGFR	Compa
!	1	!	:	!	1	1	1	!	1	1	•	1	i	1	•	1	1	1	1	1	;	1	1	1	1		1	!	IR/ICFR	risons

Figure 1F



A6S-2-B2-IGFR EMYGE	A6S-1-C5-IGFR RIHNC	16S-2-G1-IGFR RPQLV	46S-2-F1-IGFR VGQVC	A6S-4-A1-IGFR DSSRI	A6S-4-G1-IGFR AELVO	\6S-4-H1-IGFR IVAGA	A6S-3-G3-IGFR PRLHM	A6S-3-H2-IGFR QGAEC	A6S-3-E5-IGFR RYRGE	A6S-3-G10-IGFR GAVGI	A6S-4-A3-IGFR LAINÇ	A6S-4-H2-IGFR VTFTS	A6S-3-G2-IGFR TWMWE	A6S-3-H9-IGFR YSIEV	A6S-3-F8-IGFR GRGQC	A6S-4-D4-IGFR IARMF	-B4-IGFR	A6S-4-B1-IGFR RHERO	A6S-4-C1-IGFR CWARI	A6S-4-A5-IGFR VEVQI	A6S-4-A2-IGFR IGGQ	A6S-4-B2-IGFR QSVDI	A6S-4-D1-IGFR SNPSI	A6S-3-E10-IGFR RVREI	A6S-4-D3-IGFR GLRSI	A6S-4-E3-IGFR RGMT	A6S-4-A6-IGFR HVEH	Design XXXX	Clone Sequence	Ratios over Background
EMYGDTSERVNFYDWFVSAL <u>Q</u>	RIHNQTERGGNFYDWFVHQLV	RPQLVESGSKNFYDWFVQVVR	VGQVGRYVRSNFYDWFVQQAM	DSSRLWLGERNFYDWFVAQIS	AELVGAGVRGNFYDWFVDQLV	IVAGARHSEVNFYDWFVIQVR	PRLHMGSDMGDFYDWFVVQIA	<u>Q</u> GAEGRLSEGNFYDWFVQĀVS	RYRGERHDGRNFYDWFVEQVN	GAVGLAEAGPNFYDWFVSQVQ	LAINDLVTHKNFYDWFVDQLR	VTFTSAVFHENFYDWFVRQVS	TWMWEERKQDNFYDWFVGQLK	YSIEVQDWNENFYDWFVSQLG	GLKRPDNFYDWFVAAAK	IARMRETFQPNFYDWFVDQLA	ERSPRPALASNFYDWFVQQVV	RHERGKEGPGNFYDWFVSQVV	CWARPCGDAANFYDWFVQQAS	VEV <u>Q</u> RHIRKDNFYDWFVKQID	I GGQGQHQDGNFYDWFVEALA	<u>Q</u> SVDLSRPDSNFYDWFVEVLS	SNPSRQDASVNFYDWFVREVA	RVREKLPRPENFYDWFVN <u>Q</u> IH	GLRSEQGNRLNFYDWFVAQIA	RGMTGMVGRGNFYDWFVGQLR	HVEHMAVGDGNFYDWFVVQLR	XXXXXXXXNFYDWFVXXXX	nce	

30	27	30	30	17	16	18	21	21	21	24	18	19	21	23	25	18	19	19	16	19	20	21	22	23	20	21	21	;	E-Tag	Compari
ហ	7	8	æ	12	16	18	18	19	19	19	20	20	20	20	20	21	21	21	22	22	22	22	22	22	23	23	23	;	E-Tag IGFsR	SOIIS
1	1 -	1		:	:	1	1	!	;	:	!	1	:		1	1	1	!	1	1	1	ı	!	1	•	!	:	:	R	
:	1 1	1	•	1	1	!	:	•	1	1		1	1	;	1	1	!	!	1 1	•	!	!	!	•	•	1	•		IGFR/IR	
	1	1	1	!	1	-	1	1	1	1	1	) 	i i	;	;	!	!	\$ \$	:	1	1	1	!	1		1	1	:	IR/IGFR	

Figure 1F (Con't)



Ratios over Background	
Clone	Sequence
Design	XXXXXXXXXXNFYDWFVXXXX
A6S-1-D5-IGFR	RVGSGMEDLGNFYDWFVRQAQ
A6S-1-A2-IGFR	KDPVTVSQGRNFYDWFVVQIQ
A6\$-3-E6-IGFR	DARDHGVWVMSNFYDWFVAQVS
A6S-1-G3-IGFR	VATVHVGGGMNFYDWFVAQVG
A6S-3-G4-IGFR	CADPGACSSLNFYDWFVQMRG
A6S-3-H8-IGFR	NPTSVQQYGVNFYDWFVNVLS
A6S-3-E3-IGFR	RPSLPEVRPGNFYDWFVQSVR
A6S-3-D9-IGFR	SLQGADFQQGNFYDWFVSELA
A6S-2-A1-IGFR	LSSRGRVTMRNFYDWFVA <u>Q</u> VV
A6S-1-H4-IGFR	HKSWTTMSPLNFYDWFVAQVE
A6S-3-C1-IGFR	RPVIGGGGTRNFYDWFVAQMI
A6S-3-B10-IGFR	YDQDPPYWGLNFYDWFVREVA

To	17	18	31	17	19	20	21	19	20	20	25	;	Compa E-Tag
													, -
:	!	1	1	!	i i	i I	1	l i	l k	! !	1	!	R
1	1	;	1	1	1	1	1	;	† 1	1	:	1	IGFR/IR
,	) I	1	1	1 1	1	1	1	1	1	1 1	1	;	IR/IGFR

Figure 1F (Con't)



2	26.5	38.4	YPWYGGSGTYLDGAGKVASEPPARIDQQVFAGNFYDWFV	A6L-4-E11-IR
Ņ	23.6	28.6	QGGLLVTGRISDGAGKVASEPPGGIGQKVFAGNFYDWFV	A6L-4-F7-IR
22	22.6	37.1	QRGMPVLGRISDGAGKVGSEPPARIARKVFPVNFYDWFI	A6L-4-G9-IR
22	22.1	30.0	HRGMLVLGRISEGAGNVDPEPPARIGQNVFAGNFYDWFV	A6L-4-H10-IR
21	21.6	28.7	YRGQAGSGVGSLTVAGKVASDPPARIGQKVFADNFYDWFV	A6L-4-E8-IR
20	21.4	29.5	YHGKLDLGRISVGVGKVASEPPARIGQKVFADNFYDWFV	A6L-4-G2-IR
18	18.4	35.7	YRGMLVLGRISDGAGKVASEPPARIGQKVSAVNFYDWFV	A6L-4-F9-IR
17	17.5	29.0	YSGYAGSGSFSDGAGKVASEPPARISQEVLADNFYDWFV	A6L-3-A11-IR
14	14.6	38.2	QHGMLVLGRVSVGAGKVPSEPQARIGHKVFDVNFYDWFV	A6L-4-H8-IR
12	12.9	39.8	YRGMLVLGRISDGAGKVASVPPAHIGQKVFAFNFYDWFV	A6L-4-E9-IR
10	10.5	31.6	YRGMLVVGRISDGTGKVASQPPARIGQKVFAVNFYDWFV	A6L-4-F10-IR
9	9.6	35.4	QRGMLVLDRISDGAGKVASGPPARIGQNVLAVNFYDWFV	A6L-4-H11-IR
	5.7	29.5	QPWCAGSGRIYDGACKVASEPPAHIGQEVFAVNFYDWFV	A6L-3-C12-IR
۸.	4.7	37.9	<u>Q</u> RGMLVLGSISDGAGKVAYEAPARIGQTVFAVNFYDWFV	A6L-4-G8-IR
1.1	3.8	30.1	QRGMRVLGRISDGAGKVASELPPRIGQKDFAVNFYDWFV	A6L-4-E10-IR
<b>A.</b> 1	2.4	3.1	<u>Q</u> RGMLVLGRISDGAGKVAAEPPDCLGQKVCAVNFYDWFV	A6L-4-E12-IR
	2.4	21.1	QRGLLVLGRFSDGAGNVASEPPAGIGQEVFPVNFYDWFV	A6L-3-A10-IR
	2.3	32.0	YRGQLVLGRISYGAGKVGCDPPARIGQKDWAVNFYDWFV	A6L-4-G12-IR
2	2.0	27.6	VPWYAGSGSSSDGAGKVASEPPARIDQKVFAVNFYDWFV	A6L-4-G11-IR
30	27.8	33.1	YRGMLVLGRISDGAGEVASEPPARIGQEVFALNFYDWFV	A6L-3-B6-IR
23	21.8	34.7	YRGMLVLGRISDGAGKVASEPPARIGQEVFADNFYDWFV	A6L-3-C3-IR
18	16.2	38.6	FRGRLVLGHFSDGAGKVGSEPAARIGQKVFDVNFYDWFV	A6L-4-G7-IR
6	5.4	38.1	<u>Q</u> RGMLALGRISDGAGKVASEPPAGIGQKVFAFNFYDWFV	A6L-4-E4-IR
25	21.1	38.5	YRGILVLGRISEGAGKVASEPAARIGQKVFADFYDWFV	A6L-4-H4-IR
	3.5	37.5	QRGMLLLGRISDDAGKVASEPSARRGQKVFAFNFYDWFV	A6L-4-H7-IR
26	19.8	22.6	QRGMLVRGRISHGAGKIAYEPPDCLGQKACAVNFYDWFV	A6L-3-D1-IR
;	.4.0	19.0	YRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDWFV	Parental/Design
₹	IGFsR	E-Tag	Sequence	Clone
inq	Kalios over Background	Kallos ove		
_	7	J		

20.7

14.6 17.5 18.4 10.5

Comparisons IGFR/IR IR/IGFR

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Comparisons IGFR/IR IR/IGFR

Figure 1G (Con't)



		9	er Background	pun	Comparisons	isons IR/IGI
Clone	Sequence	E-Tag	IGISK	NI.	ICHAIN	
Parental/Design	YRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDWFV	19	44.	1	1	[
761 - 4 - F8 - TGFR	YRGMMVÖGRISDGAGKVASVSPVRIGQKVIAVNFYDWFV	26	28	1	1	1
0.31	VRGRI.GI.GRISDVAGKVACDPSARIGQKVLPVNFYDWFV	39	22	1	1	1
A6L-2-G9-IGER	VECMIVIGRISDGAGRVASEPOARIGOKVFAVNFYDWFV	23	22	1	t I	i I
A6L-4-E/-1GFK	OGGMI, VEGRI SDGAGKVASOPPARI GPKGFAGNFYDWFV		22	t I	;	1
Abb-4-Gio-ion	VPCMBVI.GRISDGAGKVASEPPTHIGOKVFPVNFYDWFV		21	1 F	1	!
Abb-2-Ey-1GFR	VRGMI.VI.GRISDGAGKVGSEPAARIGOKVFALNFYDWFV	34	21	i I	1	1
A6L-2-U6-IGFR	VPCOCMVI GRISDGAGKVASEPPGRIGOKVFPVNFYDWFV		21	1	1	1
A6L-3-RIZ-IGER	VRGMLGLGRITGGAGKVASEPPDRIGQHVFVDNFYDWFV	20	20	!	ı	1
261-4-B8-IGFR	DGMLVLGRISDGAGNVASEAPARIGQKVFAVNFYDWFV	20	19	l l	;	
A614-G7-IGFR	YRGMRVRGR I SDGAGKAASDPRAR I GQTVLDVNFYDWFV	19	19	1	1	1
A6L-2-D9-IGFR	YRGMWVLGRISYGAGKVAYEPPARMG <u>Q</u> KGFAVNFYDWFV	38	18	;	,	!
A6L-4-F7-IGFR	YRGMLVGGRIAGGAGIVASEPPARIGQKVFAVNFYDWFV	18	18	1	!	1
A6L-4-E12-IGFR	YRGLLGLGGISDGAGKVASEPPARNGQKVFAVNFYDWFV	15	3	1	;	!
A6L-4-H7-IGFR	YRGMLGLGRISAGAGKVASGAPARIGQEDFAVNFYDWFV	14	13	!	!	1
A6L-4-H12-IGFR	YRGMLALGRISEGAGKVASEPPARIGQNVFAVNFYDWFV	13	12	1	!	1
A6L-2-A4-IGFR	YRGMLVLGRISDGAGKVASEPPARIGQKVLAVNFYDWFV	17	4.	1	i I	!
A6L-3-D10-IGFR	YPGMLVPGRISDGAGEGATDPPPRIGQKVFAFNFYDWFV	16	4.	t 1	1 1	!
A6L-2-F6-IGFR	YRGMLVPGRISDGAGKVAYEPPARIGQKIFAVNFYDWFV	15	4.	1	1	1
A6L-2-B11-IGFR	YRGVLVLGRVSDGVGKVASEPPAHRGQRVFGVNFYDWFV	26	ω	1	1	i i
A6L-1-B7-IGFR	YRRMLVLGRISDGAANVASGPPDRIGQKVFAGNFYDWFV	23	ω	!	i 1	1
A6L-1-D8-IGFR	YRRMLALGRFSDVTGDVASEPPAHIGQKVVAVNFYDWFV	23	ω	1	1	;
A6L-0-A11-IGFR	$\mathtt{YRGMVVRGRIFDGPGKVASEPRARIGQ}\mathtt{KVFAVNFYDWFV}$	19	ω	1	1	1
w	YRGMLILGRISDGAGKVASEPPARVGQDVVAVNFYDWFV	9	ω	1	!	ı
A6L-1-G7-IGFR	YPGRLVGGRISDGVGKVASEPPGRIGQKVFAVNFYDWFV	20	2	:	1	ı,
A6L-1-B9-IGFR	QRGLLVLGRIFDGAGKVASDPPARIGQKDFADNFYDWFV	18	2	1	1	!
A6L-1-C9-IGFR	YRGMLVLGRISDGAGKVAFEPPARIG <u>Q</u> NVFAVNFYDWFV	18	2	1	1	1
0-G10	YRCMPVLGRISDGAG#VASDRPARIGQKVFAVNFYDWFV	18	ν	1	ł 1	!
A6L-1-G8-IGFR	YRGRLVLGRISDGAGKVAAEPPASMDSKVFAGNFYDWFV	15	2	i	1	:

Figure 1H



E4D0-1-B3-IR E4Dα-1-A1-IR Ę4Dα-3-E5-IR Ę4Dα-1-B8-IR Design £4Dμ-1-A10-IR Ę4Dα-1-A6-IR Ę4Dα-2-D9-IR  $E4D\alpha-3-F3-IR$ E4Da-1-A3-IR E4Dα-2-C9-IR E4Dα-1-B1-IR E4Da-1-A8-IR  $E4D\alpha-2-D6-IR$  $\mathbb{E}4D\alpha-2-D3-IR$ E4Dα-1-A9-IR  $E4D\alpha - 3 - F10 - IR$  $E4D\alpha - 3 - F4 - IR$  $E4D\alpha-2-D5-IR$  $E4D\alpha-2-C1-IR$ E4Dα-3-F8-IR  $E4D\alpha-3-E3-IR$ E4Dα-1-B4-IR GFREGYFYDWFLAQVT GFREGAFYDWFEAQVT GFREGNFYDWFEAQVT GFREGTFYDWFVAQVT GFREGQFYEWFAAQVT GFREGDFYEWFVAQV'I GFREGQRWYWFVAQVT GFREGNFYDWFVAQVT Sequence GFREGKFYQWFEAQVT GFREGAFYDWFVAQVT GFREGNFYDWFVAQVT GFREGTFYEWFVAQVT GFREGDFYDWFQAQVT GFREGQFYEWFLAQVT GFREGQFYDWFRAQVT GFREGEFYDWFQAQVT GFREGQFYDWFLAQVT GFREGQFYDWFVAQVT GFREGSFYAWFQAQVT GFREGSFYGWFQAQVT GFREGDFYQWFEAQVT GFREGYFYEWFQAQVI **GFREGIFYEWFVAQVT** 

45.3	43.1	20.9	34.6	25.9	43.8	27.8	33.2	35.1		46.9	45.3	34.0	44.1	46.9	48.9	56.3	41.8	22.9	48.7	39.6	40.7	!	Ratios ove E-Tag
6.6		16.0	4.0	7.6	23.8	4.5	5.6	16.3	14.1	41.0	40.3	8.1	31.1	41.5	42.2	51.2	38.6	ω . ω	44.9	2.0	1.0	1	er Backgrot IGFsR
2.9	5.0	7.4	1.9	3.7	11.4	2.3	2.8	8.7	8.0	22.5	22.5	4.8	19.7	26.2	26.5	32.6	26.5	2.4	31.4	1.5	12.3	1	round IR I
2.3	2.3	2.2	2.1	2.1	2.1	2.0	2.0	1.9	1.8	1.8	1.8	1.7	1.6	1.6	1.6	1.6	1. 5	1.4	1.4	1.3	0.1	1	Compar GFR/IR
0.4	0.4	0.5	Q.5	0.5	Q.5	0.5	0.5	0.5	0.6	0.5	0.6	0.6						•		•		•	Comparisons FR/IR IR/IGFR



	E4Db-4-GTO-TK
GFREGAFYDWFAAQV'	DADR A - CIO-TR
GFREGDFYDWFVAQV"	F4DB-4-B8-IR
GFREGNFYDWFVAQV"	E4Dβ-4-D12-IR
GFREGSFYNWFQAQVT	$E4D\beta-4-F10-IR$
GFREGNFYEWFTAQVI	£4Dβ-4-B9-IR
GFREGTFYDWFQAQVT	$E4D\beta-4-G11-IR$
GFREGSFYDWFGAQVT	$E4D\beta-4-A9-IR$
GFREGSFYDWFVAQVT	$E4D\beta-4-A8-IR$
GFREGEFYDWFVAQVT	$E4D\beta-4-C8-IR$
GFREGHFYDWF?AQVT	$E4D\beta-4-G7-IR$
GFREGDFYEWFEAQVT	E4Dβ-4-E8-IR
GFREGEFYEWFAAQVT	E4Dβ-4-C10-IR
GFREGTFYDWFVAQVT	E4D 3-4-B11-IR
GFREGRFYDWFVAQVT	E4Dβ-4-E10-IR
GFREGEFYEWFVAQVT	E4Dβ-4-A10-IR
GFREGKFYDWFLAQVT	E4Dβ-4-A12-IR
GFREGNFYEWFQAQVT	E4Dα-4-H2-IR
GFREGSFYDWFQAQVT	
GFREGGFYEWFQAQVT	E4Dα-3-F12-IR
GFREGVFYDWFVAQVT	E4Du-1-B2-IR
GFREGDFYGWFQAQVT	2
GFREGGFYDWFVAQVT	- 6H-
GFREGDFYQWFVAQVT	رع ا
GFREGDFYDWFVAQVT	-3-F9-
GFREGSFYDWFVAQVT	-G2-
GFREGNFYDWFAAQVT	ָּ רַ
GFREGSFYEWFQAQVT	EADY - 4 - H5 - IR
GFREGNEYDWFVAQVT	Clone
Sequence	2

38.5	35.9	41.1	7.7	27.2	28.9	35.8	31.2	35.5	30.9	28.7	27.8	36.1	9.6	5.8	41.1	37.8	40.2	38.9	39.4	42.4	47.8	26.0	36.2	23.4	47.6	47.2	1 1	Ę-Tag	Ratios ove
25.5	27.0	27.2	1.5	9.1	9.7	9.0	14.5	22.5	14.7	16.7	13.3	15.2	1.2	1.2	8.3	33.9	11.1	16.6	18.7	23.2	24.8	4.9	15.6	20.4	33.4	36.0	1	ICESK	nô.
33.7	35.2	36.1	2.1	12.5		13.1		32.9	24.7	28.2	23.7	26.9	2.2	2.4	28.7	8.2	ω ω	5.6	7.2	9.0	9.5	2.0	6.3	8.6	13.8	14.7	l l	IK I	<u> </u>
0.8	0.8	0.8	0.7	0.7	0.7	0.7	0.7	0.7	0.6	0.6	0.6	0.6	0.5	0.5	0.3	4.1	3.4	ω •	•	•		•		•			1	TATAL T	Comparisons
٠ ن	<u>ب</u> س	<u>س</u> ر ندا	1.4	1.4	1.4	) <u>1</u> .5	, p , 5	1.5	1.7	1.7	1.8	1.8	1.8	2.0		0.2	o . u	•		) C	) C	•		) , ,	> #	· +	> >	1 1	isons IR/IGFR

Figure 11 (Con't)



E4Dβ-4-B7-IR	E4DP = 4 - F7 - IR	E4DD-4-F12 IR	E4D -4 07 -TR		E4DD-4-C7-18	E4DD-4-III	E4DP-4-U12-IR	5450-4-F12-IR	E4U/3-4 V IR	7458-4-D9-IR
GFREGGFYEWF?AQVT	GFREGGFYAWFAAQVT	GFREGGFYDWFLAQVT	GFREGSFYEWFEAQVT	GFREGDFYDWFAAQVT	GFREGNFYDWFAAQVT	GFREGQFYDWFAAQVT	GFREGAFYDWFEAQVT	GFREGSFYEWFDAQVT	GFREGSFYDWFAAQVT	GFREGSFYDWFEAQVI

l I	31.0	39.3	14.8	10.9	38.7	38.0	41.2	40.2	39.3	34.1
:	22.2	31.3	5.9	4.9	33.3	22.5	27.1	27.8	35.6	19.3
1	19.5	28.3	6.1	5.6	36.6	27.6	32.3	33.4	44.4	25.7
1	<b>⊢</b> .	, h-	, ⊢		9 4			) C	· ·	0.8
-		) (	) H		I I	- F	) t	) i	ر ا	1.U



E4D-1-B5-IGFR	E4D-1B-A3-IGFR	E4D-1B-A10-IGFR	E4D-1-D4-IGFR	E4D-2-D1-IGFR	E4D-2-E2-IGFR	E4D-3-B1-IGFR	E4D-1B-C12-IGFR	E4D-3-B7-IGFR	E4D-2-F7-IGFR	E4D-2-F6-IGFR	E4D-3-G10-IGFR	E4D-3-D5-IGFR	E4D-2-F3-IGFR	E4D-1B-E5-IGFR	E4D-3-F9-IGFR	E4D-3-D8-IGFR	E4D-2-C10-IGFR	E4D-2-F4-IGFR	E4D-2-E10-IGFR	E4D-18-C4-IGFR	E4D-2-H9-IGFR	E4D-2-E5-IGFR	E4D-2-A9-IGFR	E4D-2-D10-IGFR	E4D-2-B1-IGFR	E4D-2-C11-IGFR	E4D-2-E7-IGFR	Design	Clone
GFREGTFYDWFVAQVT	GFREGDFYDWFEAQVT	GFREGHFYDWFEAQVT	GFREGYFYDWFKAQVT	GFREGHFYDWFDAQVT	GFREGDFYDWFSAQVT	GFREGHFYEWFQAQVT	GFRDGSFYDWFVAQVT	GFREGNFYDWFVAQVT	GFREGDFYQWFAAQVT	GFREGQFYDWFVAQVT	GFREGQFYDWFAAQVT	GFREGQFYEWFVAQVT	GFREGHFYDWFVAQVT	GFREGDFYDWFLAQVT	GFREGSFYEWFQAQVT	GFREGQFYEWFEAQVT	GFREGHFYDWFQAQVT	GFREGNFYDWFLAQVT	GFREGNFYDWFQAQVT	GFREGDFYDWFAAQVT	GFREGGFYDWFVAQVT	GFREGDFYDWFQAQV'I'	GFREGDFYDWFVAQV''	GFREGGFYDWFQAQVT	GFREGDFYGWFQAQVT	GFREGSFYDWFVAQVT	GFREGDFYDWFRAQVT	GFREGNEYDWFVAQVT	Sequence

19	22	23	18	24	21	21	23	23	19	24	22	22.	23.	24.	22.	21.	22.	25.	21.	24.	19.	24.	17.	20.	22.	$\mathbf{L}$	Ò	:	E-Ta	Ratio
_	_	_	_	ئر	<u>.</u>		_	۲	<b>—</b>	_	<b>_</b>	-ب	L		س	_	N	2	.0 20	N	2	2	N	2	2	2	. 8 22	,	ان ان	s over Ba
) ) )	&		.4	3.2 -		.0		. 4	7.5 -	7.5 -	7.6 -	3.0 -	.0	8	. 7	&		.2	Մ	Մ	.7 -	. 2	.5	2.1 -	2.5	2.6 -	2.8 -	•	FSR I	Ratios over Background
i	•	;	i	i	i		•		•		1	•			•		!	1	:	;	1		;	•	•	•	•	1	~	
•	:	:	:		t t	1	1	1,	;	1	1	:		;	;	:	•	•	•	;	1	1	:	!	;	1	1	;	RIR IR	Comparisons
! !	;	;	:	!	;	;	:	:	;	;	1	1	1	;	!	1	1	ŀ	:	;	:	1	!	!	;	1	1	:	/IGFR	ons



Clone  Design  E4D-1B-B8-IGFR  E4D-1-G7-IGFR  E4D-1B-A11-IGFR  E4D-1-C3-IGFR  E4D-2-H1-IGFR  E4D-1-C2-IGFR	Sequence GFREGNEYDWEVAQVT GFREGDYYGWFEAQVT GFREGDFYAWFMAQVT GFREGNFYEWFLAQVT GFREGSFYDWFDAQVT GFREGNFYDQFVAQVT
E4D-1-G7-IGER E4D-1-G3-IGER	GEREGGEVDWEDAOVT
E4D-2-H1-IGFR	GFREGNFYDQFVAQVT
Ę4D-1-C2-IGFR	GFREGHFYEWFAAQVT
E4D-18-A12-IGFR	<b>GFREGNFYEWFVAQVT</b>
E4D-1B-A1-IGFR	GFREGKFYDWFVAQVT
E4D-2-A3-IGFR	GFREGMFDVQLLAQVT

Ratios ov	Ratios over Background	Ě	Comparisons	risons	
E-Tag	IGFsR	₹	ICFIVIR INIGFR	IR/IGFR	
!	!	;	:	!	
23.8	10.7	1	ì	•	
14.3	10.5	1	† 1	!	
24.0	10.0	ı	:	1	
15.8	9.3	:	1 3	1	
19.6	4.9	:	1	1	
11.5	4.5	1	!	1	
18.4	3.5	;	1	i I	
22.5	2.9	:		, 1 1	
22 7	ر ا	1		:	

Clone

Design

QPKPGTLHENFYDWFVRQVSSSGWVG SRALAAVHEQFYDWFVRQVSGLDWGY **QPHSSRLHESFYDWFDRQVPWYALDR** GTSNHSLHENFYDWFVRQLSSVQSSG **AARTSLFHEDFYEWFDRQVRQEGMWG** <u>Q</u>RGAPKSDENFYDWFVRQVLRFGEND RGRLIQLHEDFYDWFLRQVSGMGGGS TGAEVSFHENFYDWFDRQYSSWLDRD <u>LVGDAPFHEDFYDWFARQVFGCCQEQ</u> GGGKVNFHEDFYGWFVQQFSGVGSDR QRLSLHEQFYDWFVGQVSPLGAGG TYKARFLHENFYDWFNRQVSQYFGRV SNDERQFHETFYDWFVRQVSADGADR GRQDSGLHEHFYDWFSRQVQGEVALG VSHVHLFHENFYDWFVRQLAAEGFSG SLSREQFHENFYDWFARQVSELEGVV VTFTSAVFHENFYDWFVRQVS XXXXXXFHENFYDWFVRQVSXXXXXX Sequence NGTSQALHQNFYDWFAQQISGSEPGP LSTEQRFHEKFYDWFVHQVSTSGGGT VGQSVTFHGDFYDWFDRQLSGSQEFG VSQLSDFHENFYGWFARQIAGQAEWT T<u>Q</u>KA<u>Q</u>SLDEKFYDWFVRQVSGGGLTG I PGRRSLHENFYDWFVRQVSPGGGSÅ <u>Q</u>PVSGSVHERFYDWFVRQVSGSAGGG SRGSGVFHESFYNWFDRQVSEWIQFG PNVGYAFHENFYDWFIRQVSIEEKAG  $\mathtt{TIDHHPLHEQFYDWFARQVSDLESLG}$ ASQLPPVYENFYEWFDRQVSLDAQRE



26.6	2	26.5	œ	J	7	7	42	O	$\sim$	W	7	w	w	_	٠.					•	37.1	36.0		•	31.2	•	29.8	:	Ratios ove E-Tag
	•	21.4	•	7.	9	6	5	4.	29.1	•	6	5.1	ហ •		9.	2.	4.		5.1	ა	23.3	۲.	12.1	13.4	4.4	2.2	17.5	:	over Background IGFsR II
œ	22.4	21.5	ω. <sub>5</sub>	9	9	0	7	σ	٣	32.2	9	5.6	7	36.2	2	3.2	1	25.1	9	ù	34.3	'n	2		18.8		16.3	;	IR I
1.0	1.0	1.0	•	•	0.9							0.9				0.8	•	٠	0.8		0.7	•	•	0.5	0.2	0.1	1.1	!	Comparisons GFR/IR IR/1
1.0	1.0	1.0	1.0	1.1	1	, p.	μ	1.1	سو سو	1.1	1.1	1.1	р. Н	1.2	1.2	1.2	1.6	)  - ) (.	·	عبر د 		; L , o	i .	· 1-	4. i	, 00 , N	0.9	,	isons IR/IGFR



H2CA-3-B9-IR H2CA-4-F5-IR H2CA-3-B10-IR H2CA-3-A12-IR H2CA-3-A8-IR	H2CA-4-G5-IR H2CA-4-E8-IR H2CA-4-G6-IR H2CA-3-B7-IR H2CA-3-B4-IR H2CA-3-C7-IR H2CA-4-E5-IR H2CA-4-E5-IR
RLALRTFHQDFYDWFVRQVAAEDTDP QGSFAVLHENFYDWFARQVSGVEGLA QGNMSALHENFYDWFVRQVSEADRVD VAYPALLHEQFYDWFVRQVSAVAGTT PDTINSQHKNFYDWFVRQVSGVGTSS	DRLRARFNENFYDWFDRQVSGQGSMP VLGVAQFHDKFYDWFARQVSQLESAG GVVGGAFHEQFYDWFDRQVSAAFKGD DESEMRLHEQFYDWFARLVSLEGGSA EGGGVAIHENFYDWFDRQVSLQGWSD SRIVSRFHENFYDWFVRQVSGDAPVQ IPAGAQLHENFYDWFARQVSGEDGGA GSSAAGFDEQFYDWFDRQVSEAFRDG

36.8	37.8	41.9	38.8	39.4	39:7	37.3	40.2	39.8	37.6	36.2	35.7	35.3	39.5	33.3	35.9	35.5	36.6	36.9	38.1	37.9	35.3	33.0	38.9	33.9	34.1	38.3	36.6	:	E-Tag	Ratios ov
22.5	7.3	38.9	38.0	37.7	37.6	37.0	36.7	36.5	36.5	35.0	•	34.0	•	33.0	33.0	32.8	32.7	32.3	32.0	31.9	31.4	31.1	31.1	31.0	30.7	30.7	30.6	•	IGFsR	Ratios over Background
19.2	6.3	38.0	37.8	37.6	37.6	36.3	35.9	35.1	35.3	33.5	34.9	35.6	33.7	32.9	33.4	33.3	32.5	31.6	31.9	31.0	30.0	29.8	31.4	31.8	30.4	31.0	30.9	:	₽	und
1.2	1.2	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	!	<b>IGFIVIR</b>	Compa
0.9	0.9	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	•	IIVIGER	Comparisons

Figure 1K (Con't)



H2CA-3-C11-IR H2CA-3-C4-IR H2CA-4-E6-IR H2CA-3-D7-IR H2CA-3-A7-IR H2CA-3-A7-IR H2CA-3-D1-IR H2CA-3-C1-IR H2CA-3-D8-IR H2CA-4-H4-IR H2CA-4-F6-IR H2CA-4-E4-IR H2CA-3-A6-IR
H2CA-4-E9-IR
H2CA-4-F3-IR
H2CA-4-H6-IR
H2CA-4-H2-IR
H2CA-4-H2-IR H2CA-4-E3-IR H2CA-3-B5-IR H2CA-4-E1-IR Design H2CA-3-D12-IR H2CA-4-E12-IR H2CA-3-D3-IR H2CA-4-H12-IR H2CA-3-D11-IR H2CA-3-D6-IR FGRGVHCDENFYDWFVCQVSGALLEG ETPLTELHEQFYDWFVRQVSGFPGGV XXXXXXFHENFYDWFVRQVSXXXXXX SEDVDSRHENFYDWFVRQVSGIGLQD PAPADAFDHNFYDWFARQLSATTTIQ GHORDLLHESFYDWFVRQVSEAEGGG GYAVCQYQANFYDWFVRQVDGMSNGG ANOMGREHDNEYDWEDRQVSRYERGT VPDAQIFHESFYDWFVRQASAGGPAD VFERSRCHDNFYDWFFCQVSGQADGG QGGLGDFDEDFYDWFARQVSRRDRAD SPEGNLVHDQFYDWFVRQLSSTSAGT GAGGRDFDEDFYDWFVRQVSGQVTSG RSEQYRFHENFYEWFDRQVSRMGLLG <u>Q</u>HRGPHFHEDFYDWFVRQVSSAVPSD PDAEKQFHETFYGWFVRQISEDSANS GNVRGQFHGQFYDWFARQVSGSEGDA MVQRISIHENFYDWFVRQISGSAVPP ERTAETLHEQFYDWFVRQVSAMDGES DRPSSFIHENFYEWFARQVSQSGSSG **QAVTRRFHENFYDWFARQVSEEGGWS** PSRKDGLHQSFYDWFARQVQDMEGRA LLASRAFHENFYDWFARQVSGTQPPG RNWNLQFNENFYDWFDRQVSALRGGG **QAAVGVCNKDFYAWFACQVREDFAKA** RODPGLFHONFYDWFDRLVSAWDGOE PDRSDRLDDNFYDWFVRQVSQVINED LTSQLLSHEDFYDWFVRQVSGVGGSG LSQGVGFQENFYEWFERQVSGWDGRD

	38.1	40.0	39.4	37.6	35.3	42.5	39.3	41.9	40.3	38.6	38.7	38.5	37.8	39.9	34.5	38.7	41.8	37.1	41.0	38.8	34.0	•	33.3	33.1	29.8	38.8	36.8	;	E-Tag	Ratios ov	
	32.9	38.4	36.2	19.4	15.2	39.2	38.8	38.4	38.3	38.0	37.5	37.0	36.7	36.1	35.5	35.5	35. <b>3</b>	34.5	34.2	33.7	33.1	32.4	32.3	29.9	12.5	35.2	34.1	:	ICF5R	Ratios over Background	
	27.2	29.3	27.6	15.1	11.6	35.5	35.8	35.0	36.1	34.7	35.2	33.7		32.9	31.3	• .	32.8	•	32.0	•	•	29.4	30.2	27.5	11.3	30.5	29.6	:	₹	bau	
	1.2	1.3	1.3	1.3	1.3	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.2	1.2	;	ICHVIK	Comparisons	
,	0.8	0.8	0.8	0.8	0.8	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	:	IKICER	risons	

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Figure 1K (Con't)

38.5

38.4

31.7

1.2



H2CA-3-B8-IR	H2CA-3-C6-IR	H2CA-4-G7-IR	Design	Clone
RQGHAGFHDNFYDWFVRQVSGSTPQV	ADCYVQLHENFYDWFRRQVCNLQEGM	RAGGVGLHDNFYDWFVRQVSGGDSGP	XXXXXXFHENFYDWFVRQVSXXXXXX	Sequence

,	
	1.5
	28.2



LGYQEPFQQNFYDWFVRQVSGAENAG	4
RGAVAGFHDQFYDWFDRQVSRVHKFG	H2CA-4-H9-IGFR
DERGGKFREDFYDWFVRQVSESRFGQ	H2CA-3-D11-IGFR
SRVTTVFHENFYDWFVRQLSDSAISG	H2CA-4-F2-IGFR
RSASGSLPEQFYDWFVRQVSLSGTDK	H2CA-3-D4-IGFR
GAPVDQLHEDFYDWFVRQVSQAATG	H2CA-2-B2-IGFR
PPLASDLDVQFYGWFVQQVSPPGRGG	H2CA-2-B3-IGFR
CCLLCRFQQNFYDWFVCQGISRLRPL	H2CA-2-B4-IGFR
RCGRELYHSTFYDWFDRQVAGRTCPS	H2CA-1-A7-IGFR
LRRQAPVEENFYDWFVRQVSGDRVGG	H2CA-3-D7-IGFR
FYVQQWGHENFYDWFDRQVSQSGGAG	H2CA-4-F1-IGFR
TLDGGSFEEQFYDWFVRQLSYRTNPD	H2CA-4-G11-IGFR
NYRRQVFNGNFYDWFDRQVFSLVTPG	H2CA-3-D8-IGFR
QSPVGSSHEDFYDWFFRQVAQSGAHQ	H2CA-3-D6-IGFR
SSIGGGFHENFYDWFSRQLSQSPPLK	H2CA-4-F7-IGFR
QAVQPGFHEEFYDWFVRQVSTGVGGG	H2CA-4-H4-IGFR
RAGSSDFHEDFYEWFVRQVSLSLKGK	H2CA-2-B9-IGFR
SSCDGAGHESFYEWFVRQVSGCRSV	H2CA-3-C8-IGFR
APDPSDFQEIFYDWFVRQVSRMPGGG	H2CA-1-A3-IGFR
VNQSGSIHENFYDWFERQVSHQRGVR	H2CA-4-F10-IGFR
AVRATRFDEAFYDWFVRQISDGQGNK	H2CA-4-F6-IGFR
SAAQLFFQESFYDWFLRQVAESSQPN	H2CA-4-F11-IGFR
SACQFDCHENFYDWFARQVSGGAAYG	H2CA-4-H8-IGFR
VGYQGQGDENFYDWFIRQVSGRLGVQ	H2CA-4-F-IGFR5
VGRASGFPENFYDWFGRQLSLQSGEQ	H2CA-4-H6-IGFR
GIISQSCPESFYDWFAGQVSDPWWCW	H2CA-4-G9-IGFR
VTFTSAVFHENFYDWFVRQVS	Parental
XXXXXXFHENFYDWFVRQVSXXXXXX	Design
Sequence	Clone

8.3 10.9 10.8 5.8 13.3 8.0 3.5 7.7 4.1 17.6 9.3 12.2 8.7 11.9	Ratios ov E-Tag 29.8 8.6 4.9 5.5 5.6 3.9 4.9 7.7 7.7 15.1 9.3
9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0	Ratios over Background E-Tag IGFsR IR 29.8 17.5 16 8.6 9.5 0 4.9 10.5 0 5.5 9.7 0 5.6 9.2 1 3.5 6.8 1 3.9 7.3 1 4.9 5.7 1 7.7 3.8 0 15.1 5.6 1 9.3 7.0 1 9.3 7.0 1 1.5 3.2 0
2	
4 4	Comparisons IGFR/IR IR/IGFR  1.1 0.9 16.0 0.1 14.6 0.1 12.3 0.1 9.4 0.1 6.7 0.1 6.7 0.1 6.4 0.2 5.9 0.2 5.1 0.2 4.8 0.2 4.2 0.2 4.1 0.2
	1RVIGFR  0.9 0.1 0.1 0.1 0.1 0.1 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2



Sequence  XXXXXXFHENFYDWFVRQVSXXXXX  WRGHGTFHEDFYDWFVRQVSGSGSST  GGRVGVLHENFYDWFDRQVSLRGADG  CNLTAGFHEQFYHWFAIQVCGDAENA ERGEDMFHENFYDWFVRQISGRQGGG  TNQGVGFYDSFYGWFVRQISSRCNDC  HLADGQFHEKFYDWFERQISSRCNDC  QTFGKSLHENFYDWFDRQVSGAAGER  FRTLAAQHDSFYDWFDRQVSGAQKIL
--

Ratios ov E-Tag	Ratios over Backgrou E-Tag IGFsR	und IR	Compa IGFR/IR	arisons R/IGFR	
;	1	;	:	;	
15.7	8.7	3.1	2.8	0.4	
11.5	7.4	3.0		0.4	
9.4	6.8	2.9	2.3	0.4	
12.5	6.4	2.8	2.3	0.4	
18.0	6.2	2.7	2.3	0.4	
4.7	2.2	1.0	2.2	0.5	
9.8	9.9	4.8	2.1	0.5	
9.3	ω . <b>ω</b>	1.6	2.1	0.5	
14.6	7.9	ა . 9	2.0	0.5	



H2CBα-3-C12-IR VGVNRQFHTRFYAWFDEQLGG	H2CBa-3-H7-IR GDGLTAFHQGFYEWFDIQMYG	H2CBα-3-F12-IR GFNTGTFHDQFYYWFWEAAGG	H2CBα-3-H1-IR VAVAWGLHESFYAWFENQFSD	H2CBα-3-A1-IR PGNRPTFHAEFYRWFREAQGS	H2CBα-3-B11-IR GADTGAVHRRFYLWFEQLSGG	H2CBα-3-G5-IR SRGLGLYHSGFYGWFERQFNQ	H2CBα-3-E4-IR QSFVTSVHTRFYAWFASALEM	H2CBα-3-G3-IR VVPKAGFHEAFYEWFRRQDRD	H2CBa-3-C3-IR VVGPLDIHERFYGWFHQQGGA	H2CBa-3-C1-IR IMWPCTFQDPFYCWFQTEQGR	H2CBa-3-D3-IR LVVGRRFHQSFYDWFVAAAGG	H2CBα-3-G4-IR SAKTPVLHDGFYMWFEAQSES	H2CBα-3-E11-IR GSVDREIHGPFYSWFSEQLWG	H2CBu-3-F8-IR DSVNSDLHRAFYGWFAEQWRA	H2CBα-3-B1-IR SRFDERLHHQFYEWFRVLNEP	H2CBa-3-A6-IR QFSAGAFHGDFYGWFRALYNG	H2CBα-3-G11-IR SGSRPVFHEQFYEWFVDQLG	H2CBu-3-B6-IR VGDFCVSHDCFYGWFLRESMQ	H2CBα-3-H5-IR QARVGNVHQQFYEWFREVMQG	H2CBa-3-D12-IR VASGHVLHGQFYRWFVDQFAL	H2CBu-3-D2-IR WTDVDGFHSGFYRWFQNQWER	H2CBα-3-B12-IR QSDSGTVHDRFYGWFRDT*A	Parental VTFTSAVFHENFYDWFVRQVS	Design XXXXXEHXXEIXMEXXXXAX
REYAWEDEQLGG	3FYEWFDI <u>Q</u> MYG	<u>PFYYWFWEAAGG</u>	SFYAWFENQFSD	FYRWFREAQGS	≀FYLWFEQLSGG	SFYGWFERQFNQ	REYAWEASALEM	\FYEWFRRQDRD	REYGWEHQQGGA	»FYCWFQTEQGR	FYDWFVAAAGG	FYMWFEAQSES	FYSWFSEQLWG	⊾FYGWFAEQWR,A	FYEWFRVLNEP	FYGWFRALYNG	FYEWFVDQLG	FYGWFLRESMO	PYEWFREVM <u>Q</u> G	FYRWFVDQFAL	FYRWFQNQWER	FYGWFRDT*A	NEYDWFVRQVS	FYXWFXXXXXX

26.0	21.0	21.1	27.2	31.3	28.0	26.7	28.8	23.7	23.3	27.0	23.6	24.9	14.0	23.0	33.4	25.9	22.7	31.4	16.7	24.6	20.6	26.0	29.8	•	Ratios E-Tag
12	9.7	0	10	11	œ	J	œ	0	_	ហ	N	2	2	4	6	L	<b></b>	2	2	2	1	_	17.5	t 1	over Backg IGFsR
	19.1																6		. 15	•	12.1	20.4	16.3	;	round IR
0.5		0.5																		0.1	0.1	0.1	1.1	;	Compa IGFR/IR
1.9	2.0	2.1	2.2	2.2	2.3	2.5	2.6	2.6	2.8	2.9	3.1	3.2	4.0	4.1	4.3	4.3	. 4.7	5.6	6.3	6.7	7.0	16.0	0.9	;	risons IR/IGFR

Figure 1M



GLG1ASFHEGFYSWFTAQLGA	H2CBQ-3-E3-1K
GGVSGVLHDRFYSWFERQLAG	H2CBα-3-G1-IR
VSATVMLHREFYDWFGLQLLD	H2CBα-3-C5-IR
<b>FAFGLGFHQGFYDWFAHQLEG</b>	H2CBα-3-G7-IR
PSLSSNLHESFYRWFDQLVST	H2CBα-3-G6-IR
<u>ARLLNIFDRGFYNWFQRQLDE</u>	H2CBα-3-F3-IR
VRHPTRFHDEFYRWFTEQLTT	H2CBα-3-A2-IR
AFVSERVN <u>Q</u> RFYDWFRU <u>Q</u> MRS	H2CBα-3-F5-IR
GGSSQAFHGAFYEWFSAQLRG	H2CBα-3-H6-IR
SGSRPVFHEQFYEWFVDQLGL	H2CBα-3-F9-IR
QRGGGGFHEGFYSWFRSQSLL	H2CBα-3-B7-IR
SDDSSTLNGRFYTWFHMQLLD	H2CBα-3-H4-IR
FHRPGSFNTNFYQWFDD <u>Q</u> MN <u>Q</u>	H2CBα-3-A7-IR
PSPNAPFHGGFYDWFDWVQGS	H2CBα-3-D4-IR
SEERKKVHSQFYSWFDR <u>Q</u> LLG	H2CBα-3-F6-IR
MRORDGFNSSFYGWFAAALGE	H2CBα-3-C2-IR
<u>Q</u> SGNRGSHGAFYSWFRDVLAN	H2CBα-3-E10-IR
<b>DEGGAPLDVMFYRWFEQAVRG</b>	H2CBα-3-H11-IR
PRNEGLVHGLFYDWF <u>Q</u> RALSG	H2CBα-3-B8-IR
WGPFSVFDESFYRWFAQASDD	H2CBα-3-C4-IR
FSGWADYQSGFYQWFAEELAN	H2CBα-3-A5-IR
LGGYCGFNCQFYRWFDNLADR	H2CBu-3-A10-IR
LGTLAVFHELFYGWFER <u>Q</u> LGG	H2CBα-3-H12-IR
GPRGQRLHDAFYSWFDALRVN	H2CBα-3-D11-IR
XXXXXXFHXXFYXWFXXXXXX	Design
Sequence	Clone

24.2	26.9	26.4	24.4	24.9	16.3	30.7	29.4	24.8	26.1	28.6	27.2	29.1	29.0	27.3	28.4	27.7	28.8	25.6	30.7	28.3	27.1	27.4	27.8	;	Ratios ov Ę-Tag
17.2	21.5	21.2	18.7	21.0	6.7	22.5	22.0	21.6	19.1	18.0	20.1	19.4	18.9	14.5	17.0	14.3	14.0	11.3	17.2	16.1	13.2	7.2	13.0	;	Ratios over Background E-Tag IGFsR II
19.3	26.3	25.4	23.0	24.4	9.0	29.1	27.8	27.3	24.3	23.6	27.9	26.9	27.1	•	26.7	23.0	22.4	18.6	29.2	28.1	22.3	12.4	24.8	;	und IR
0.9	0.8	0.8	0.8	0.9	0.7	0.8	0.8	0.8	0.8	0.8	0.7	0.7	0.7	0.7	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.5	:	Comparisons IGFR/IR IR/IGFR
1.1	1.2	1.2	1.2	1.2	1.3	1.3	1.3	1.3	1.3	1.3	1.4	1.4	1.4	1.5	1.6	1.6	1.6	1.6	1.7	1.7	1.7	1.7	1.9	;	risons IR/IGFR

Figure 1M (Con't)



H2CBα-3-F10-IR GRI	H2CBα-3-D10-IR ED	H2CBα-3-D5-IR LG	H2CBα-3-F2-IR VA	H2CBα-3-H8-IR LG	H2CBα-3-H9-IR VH	H2CBα-3-C6-IR LG	H2CBu-3-G8-IR WA	H2CBα-3-F7-IR GVI	H2CBα-3-G12-IR GA	H2CBα-3-E1-IR IG	H2CBα-3-B10-IR GI	H2CBα-3-C9-IR SC	H2CBα-3-A12-IR GSI	H2CBa-3-G9-IR RN:	H2CBa-3-C7-IR ARI	H2CBα-3-B5-IR HS0	H2CBα-3-E2-IR RV	H2Cβα-3-D7-IR PD:	H2CBα-3-G10-IR GAI	H2CBα-3-F11-IR VL	H2CBα-3-B4-IR EG	H2CBα-3-Cll-IR GG	H2CBα-3-A9-1R RV	Design XX	Clone Sec
GRDNMKFHSGFYDWFT <u>QQ</u> LAG	EDSRLRLHEGFYGWFRKQLGD	LGYIGALNTQFYSWFADLVGS	VARGSSLHDDFYEWFASQLRT	LGLMAIFDRGFYGWFEQQLSG	VHSVSRLNVGFYQWFQDQLSG	LGQLAAFHLGFYEWFSEAVAA	WAGRAGIHGGFYEWFNKQLRG	GVDVTDFHKDFYSWFQRQLNG	GAAGISFHRGFYDWFAAQVRD	IGPPGSLHRGFYDWFAEQVEA	<b>GIAVQSLHDSFYRWFDNALGS</b>	SCTGRQFDGCFYAWFEDQLVG	GSMSPVFNDQFYGWFRDLVDE	RNSSGNFHDKFYNWFEAQLKG	<u>ARLLERFQDPFYEWFETLMGD</u>	HSGMRDVHARFYSWFSEQLSG	RVYKANFHNEFYGWFREQLLG	PDSFMSLHQRFYSWFQAQVGT	GALSDRYNNVFYDWFREQLLG	VLLPGVVHGGFYDWFSR <u>Q</u> LSS	EGARQGFHARFYSWFAQ <u>Q</u> LAL	GGAGRSFHDAFYEWFER <u>O</u> MAG	RVDĄĄĄĻNAGFYEWFRGVIQG	XXXXXX <u>FH</u> XX <u>FY</u> XWFXXXXXX	Sequence

Ratios over E-Tag	Backg	round	Compar IGFR/IR	Comparisons FR/IR IR/IGFR
:	:	:	:	•
30.5	21.7	24.1	0.9	1.1
26.4	21.8	23.2	0.9	1.1
30.9	22.0	24.3	0.9	1.1
24.5	22.5	23.9	0.9	1.1
28.3	23.6	27.1	0.9	1.1
31.4	23.6	25.3	0.9	1.1
26.8	24.0	25.7	0.9	1.1
28.7	25.0	26.4	0.9	1.1
30.0	25.2	28.7	Q.9	1.1
7.	25.2		0.9	1.1
•			0.9	1.1
32.1	28.7		0.9	1.1
w ·	30.8	Ē	0.9	1.1
•		29.0	1.1	1.0
29.1	•		1.1	1.0
23.2	20.7	20.3	1.0	1.0
22.8	20.9		1.0	1.0
26.7			1.0	1.0
	22.5	22.0	1.0	1.0
	23.4	ω.	1.0	1.0
25.5	24.3	25.2	1.0	1.0
	24.5	S	1.0	1.0
26.8	•	24.9	1.0	1.0
51	5	9	1.0	1.0



ANDCLGLHAGFYGWFACQLGG	H2CBα-3-A3-IR
SNIEEHFHMOFYRWFSDALGN	H2CBα-3-A11-IR
RPSSGGLHYGFYHWFRVQEEM	H2CBα-3-F1-IR
VSRYGG <u>Q</u> QDGFYHWFSDLLKG	H2CBα-3-D8-IR
MRSEASFHVEFYSWFEEQLRS	H2CBα-3-B9-IR
PGAAEGFHSAFYDWFAQAVSG	H2CBα-3-D1-IR
SSNTVGLDERFYAWFVDQLGA	H2CBα-3-A4-IR
PTVHRAFDDLFYGWFAKQVED	H2CBα-3-C8-IR
SSDVGAFHSAFYDWFKAQLSG	H2CBα-3-E7-IR
SPARRVSHHDFYGWFAKQLES	H2CBα-3-E6-IR
RGRASTFHDGFYGWFSQQLRF	H2CBα-3-E5-IR
GSNGGGVHGQFYAWFVEALSG	H2CBα-3-E8-IR
<b>DLASHGFHDAFYNWFSVQLNS</b>	H2CBα-3-B2-IR
AGGRKPFHDDFYGWFRDQLAE	H2CBu-3-G2-IR
GSRQEADHQAFYDWFNLVLGV	H2Cβα-3-H10-IR
PVGIGGLHRAFYQWFQSQVDA	H2CBu-3-E9-IR
FVQNIGFDYDFYGWFVREVEK	H2CBα-3-F4-IR
<b>AGHVGQVYDGFYGWFREQLGA</b>	H2Cβα-3-H3-IR
AGVMGGFHQEFYLWFERALSN	H2CBu-3-D6-IR
XXXXX <u>FH</u> XX <u>FY</u> X <u>WF</u> XXXXXX	<b>Design</b>
Sequence	Clone

30.4	20.5	28.8	26.3	33.2	32.9	32.2	31.9	30.4	29.6	33.0	31.5	29.4	29.1	26.9	31.6	31.2	27.0	27.9	. 1	Ratios over E-Tag
29.6	21.5	28.0	20.2	33.8	32.5	31.9	31.2	30.2	29.0	28.7	28.4	28.1	28.1	27.9	27.7	27.2	26.9	26.0	:	er Background IGFsR II
21.8	17.7	26.4	19.1	33.3	31.5	32.6	31.5	30.2	28.1	28.9	29.1	28.2	28.8	28.8	28.2	27.7	26.2	25.8	;	iR
1.4	1.2	1.1	1.1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	:	Compar IGFR/IR
0.7	0.8	0.9	0.9	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	:	risons IR/IGFR



DRGRMGVDEGFYNWFARQMQE	H2CBβ-4-H1-IR
QASDNRSDGQFYLWFEKLLSS	H2CBβ-4-G6-IR
HKRGIVQHGAFYAWFDSLLSG	H2CBβ-4-H4-IR
GGAQISFHERFYQWFLQEAAG	H2CB }-4-F10-IR
CPDROSVDDRFYNWFADALAS	H2CBβ-3-C8-IR
GAMEPDYHRSFYQWFAAALGE	H2CB(}-4-G4-IR
HRVARAFHE <u>Q</u> FYDWFEKAVSG	H2CB(β-4-F2-IR
<b>ELQARGVHRNFYRWFEAQVSG</b>	H2CBβ-3-E5-IR
AVGTLGYHSGFYRWFERQLGG	H2CB }-4-F11-IR
PPGMNGFHTSFYSWFVDQLGD	H2CB }-4-F4-IR
<b>GARGSTFHDQFYEWFWVQLGD</b>	H2CB }-4-G12-IR
SVPRGTVHDAFYQWFREVALG	H2CB[3-3-E6-IR
NGQSSRFHTAFYDWFAAQLSG	H2CB }-3-D5-IR
CVAQGGFQSSFYCWFAGLDID	H2CB }-3-C4-IR
VLTSNTLHQRFYSWFAAARRE	H2CB }-4-F8-IR
TGHRLGLDEQFYWWFRDALSG	H2CBβ-3-E8-IR
XXXXXXFHXXFYXWFXXXXXX	Design
Sequence	Clone

E Ton	er Backgro		avasələr İsdinöə	IB/ICED	
: 0	:	1	: .	!	
15.9	1.9	11.8	0.2	6.1	
13.4	0.8		0.3	3.4	
21.1	1.3		Q.3	3.1	
14.0	ນ. ນ		0.3	3.1	
5.7	0.7		0.3	3.1	
6.8	1.8		0.3	3.1	
17.9	1.9		0.3	3.0	
15.0	1.7		0.3	2.9	
17.0	1.8	5.0	0.4	2.8	
15.9	1.3	3.4	0.4	2.6	
8.7	1.4	3.5	0.4	2.6	
4.9	1.4	3.2	0.4	2.3	
10.2	1.0	2.4	0.4	2.3	
20.8	4.2	9.5	0.4	2.3	
14.5	5.6	8.5	0.7	1.5	
17.0	10.1	13.2	0.8	1.3	

Figure 1M (Con't)



gn -3-D2-IGFR -3-D2-IGFR -3-B11-IGFR -4-E2-IGFR -3-A5-IGFR -4-G12-IGFR -3-B2-IGFR -3-B6-IGFR -3-B6-IGFR -4-F7-IGFR -4-G8-IGFR -4-E6-IGFR -3-D5-IGFR -4-E6-IGFR -4-H12-IGFR -4-H12-IGFR -4-G11-IGFR -4-G11-IGFR -4-G11-IGFR -4-G11-IGFR -4-G11-IGFR -4-G11-IGFR -4-G11-IGFR	H20	н2СВ	H2C	H2C	. Н2С	H2C	H2C	н2СВ	H2C	H2C	H2C	H2C	H2C	H2C	н2СВ	н2СВ	н2СВ	H2CB-	н2СВ	Par	Desig	Clone						
IGFR -IGFR IGFR IGFR IGFR IGFR IGFR IGFR IGFR	-4-H4	-3-B7	-3-B9	-4-G1	4-	-4	4	Ü	-4	-3-A6	-3-C2	-4-E6	-3-D5	-3- <b>p</b> 4	-4-G8	-4-F7	-3-B6	3-D1	-3- <del>8</del> 2	- 4	ٺ	-4-Ę2	ů	-3-C1	-3- <b>D</b> 2	ental	ign	ē
TASQECFDDGFYGWFRAWRCT SLDWRWSEEPFYRWFQRALAG CMSLSDCHRKFYGWFRAWRCT SLDWRWSEEPFYRWFQAAVGC PRSATMSDGGFYWWFASQLGL LRRSSVFHDPFYE*ISRLVGG ARLQQQFHGGFYEWFRAQVSP AQLDNLCHEPFYSWFCAVTRE WTCDTAFHQDFYQWFCDKLGV GKEGFGLDRDFYCWFRRQVQS GRAPSSFDCDFYCWFRRQVQS ISVTAVFHDGFYGWFREQLGP GPLGDGCQDGFYGWFREQLGS ISVTAVFHDFYGWFREQLGP GPLGDGCQDGFYGWFRAQVSK NSEHGRLDVDFYGWFRAQVSK NSEHGRLDVDFYGWFRAQLSG ASEPGGYLDPFYGWFRQLSG ASEPGGYLDPFYGWFRQQLSG ASEPGGYLDPFYGWFRQQLRQ RTSPGSLHNDFYGWFAQQLAR ANVSMWIQVGFYDWFDAQLRQ RTSPGSLHDPFYDWFQQLGG GGSMGGMHGSFYSWFREQLNG CLANSEDHDSFYGWFRQQLGG GGSMGGMHGSFYSWFRDAVAG	-	IG		Ţ	2-IGFR	Ţ.	1-IGFR	ī	1											2-IGFR	- IGFR		1-IGFR	-IGF	IGF			
	RPQGGSIHAGFYQWFRDAVAG	GGSMGGMHGSFYEWFALQLRS	CLANSEDHDSFYGWFCQALGG	PGVMSSFHGGFYSWFREQLNG	RTSPGSLHDPFYDWFQQQLGG	ANVSMWIQVGFYDWFDAQLRQ	<b>ASKGSSLHNDFYGWFAQQLAR</b>	NRGDGGVHSGFYNWFRLQLSG	ASEPGGYLDPFYGWFREQLRA	KRSAYNFHDPFYDWFRMQLSG	<u>GPLGDGCQDGFYGWFMCQVST</u>	NSEHGRLDVDFYGWFARVIQQ	ISVTAVFHDGFYGWFNEQVSK	DVEAETQHRLFYAWFLSQLGS	GRAPSSFDCDFYCWFRNQVQS	GKEGFGLDRDFYWWFREQLGP	WTCDTAFHQDFYQWFCDKLGV	AQLDNLCHEPFYSWFCAVTRE	ARLQQQFHGGFYEWFRAQVSP	LRRSSVFHDPFYE*ISRLVGG	PRSATMSDGGFYWWFASQLGL	LALCRRSPGSFYGWFQAAVGC	CMSLSDCHRKFYGWFKSQGGE	SLDWRWSEEPFYRWFQRALAG	TASQECFDDGFYGWFRAWRCT	VTFTSAVFHENFYDWFVRQVS	XXXXXXFHXXFYXWFXXXXXX	Sequence

Α.	٠	•	7.	5	5	7.	w	6.	8	9.	-	1.	0	2.	6.	1.		ω ·	8.	2	•	•	22.9	29.8	;	Katios ove E-Tag	;
Ψ	Û.	4.	•	5.	5	7.	8.	9.	٧.	ა	•	•	•	• '	•	•	•	•	•		•	19.6	18.6	17.5	•	Backg IGFsR	
Û.	•	•	•	5		7.	8	8		•	•	•	•	•	•	•	•	19.4	22.6	16.5	11.9	13.0	11.8	16.3	!	IR IR	•
1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.1	1.1	1.1	1.1	1.1	1.1	1.2	1.2	1.2	1.2	1.2	1.3	1.4	1.5	1.6	1.1	;	IGFR/IR I	
1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.9	0.9	0.9	0.9	0.9	•	•	•	. 0.8	0.8	0.9	0.8	0.7	0.7	0.6	0.9	:	R/IGFR	•
	.0 23.2 23.5 1.	5.6 23.3 23.7 1.0 1. 4.0 23.2 23.5 1.0 1.	5.1 24.6 24.2 1.0 1. 5.6 23.3 23.7 1.0 1. 4.0 23.2 23.5 1.0 1.	7.8 24.9 24.7 1.0 1.1 5.1 24.6 24.2 1.0 1.1 5.6 23.3 23.7 1.0 1.1 4.0 23.2 23.5 1.0 1.1	5.3     25.4     25.3     1.0     1.       7.8     24.9     24.7     1.0     1.       5.1     24.6     24.2     1.0     1.       5.6     23.3     23.7     1.0     1.       4.0     23.2     23.5     1.0     1.	5.5     25.5     24.6     1.0     1.1       5.3     25.4     25.3     1.0     1.1       7.8     24.9     24.7     1.0     1.1       5.1     24.6     24.2     1.0     1.1       5.6     23.3     23.7     1.0     1.1       4.0     23.2     23.5     1.0     1.1	7.1 27.5 27.3 1.0 1.0 5.5 25.5 24.6 1.0 1.0 5.3 25.4 25.3 1.0 1.0 7.8 24.9 24.7 1.0 1.0 5.1 24.6 24.2 1.0 1.0 5.6 23.3 23.7 1.0 1.0 4.0 23.2 23.5 1.0 1.0	3.9     28.3     28.1     1.0     1.1       7.1     27.5     27.3     1.0     1.1       5.5     25.5     24.6     1.0     1.1       5.3     25.4     25.3     1.0     1.1       7.8     24.9     24.7     1.0     1.1       5.1     24.6     24.2     1.0     1.1       5.6     23.3     23.7     1.0     1.1       4.0     23.2     23.5     1.0     1.1	6.8       29.0       28.1       1.0       1.0         3.9       28.3       28.1       1.0       1.1         7.1       27.5       27.3       1.0       1.1         5.5       25.5       24.6       1.0       1.1         5.3       25.4       25.3       1.0       1.1         7.8       24.9       24.7       1.0       1.1         5.1       24.6       24.2       1.0       1.1         5.6       23.3       23.7       1.0       1.1         4.0       23.2       23.5       1.0       1.1	8.8     12.2     10.8     1.1     0.9       6.8     29.0     28.1     1.0     1.0       3.9     28.3     28.1     1.0     1.0       7.1     27.5     27.3     1.0     1.0       5.5     25.5     24.6     1.0     1.0       5.3     25.4     25.3     1.0     1.0       5.3     24.9     24.7     1.0     1.0       5.1     24.6     24.2     1.0     1.0       5.6     23.3     23.7     1.0     1.0       4.0     23.2     23.5     1.0     1.1	9.6 15.8 14.8 1.1 0.1 8.8 12.2 10.8 1.1 0.1 6.8 29.0 28.1 1.0 1.0 3.9 28.3 28.1 1.0 1.0 7.1 27.5 27.3 1.0 1.0 5.5 25.5 24.6 1.0 1.0 5.3 25.4 25.3 1.0 1.0 7.8 24.9 24.7 1.0 1.1 5.1 24.6 24.2 1.0 1.1 5.6 23.3 23.7 1.0 1.1 4.0 23.2 23.5 1.0 1.1	1.4     17.9     16.4     1.1     0.9       9.6     15.8     14.8     1.1     0.9       8.8     12.2     10.8     1.1     0.9       6.8     29.0     28.1     1.0     1.0       3.9     28.3     28.1     1.0     1.0       7.1     27.5     27.3     1.0     1.0       5.5     25.5     24.6     1.0     1.0       5.3     25.4     25.3     1.0     1.0       5.3     25.4     25.3     1.0     1.0       5.1     24.9     24.7     1.0     1.0       5.1     24.6     24.2     1.0     1.0       5.1     24.6     24.2     1.0     1.0       4.0     23.3     23.7     1.0     1.	1.9     18.3     16.9     1.1     0.9       1.4     17.9     16.4     1.1     0.9       9.6     15.8     14.8     1.1     0.9       8.8     12.2     10.8     1.1     0.9       6.8     29.0     28.1     1.0     1.0       3.9     28.3     28.1     1.0     1.0       7.1     27.5     27.3     1.0     1.0       5.5     25.5     24.6     1.0     1.0       5.3     25.4     25.3     1.0     1.0       5.1     24.9     24.7     1.0     1.       5.1     24.6     24.2     1.0     1.       5.6     23.3     23.7     1.0     1.       4.0     23.2     23.5     1.0     1.	0.2     18.6     16.5     1.1     0.9       1.9     18.3     16.9     1.1     0.9       1.4     17.9     16.4     1.1     0.9       9.6     15.8     14.8     1.1     0.9       8.8     12.2     10.8     1.1     0.9       6.8     29.0     28.1     1.0     1.0       3.9     28.3     28.1     1.0     1.0       7.1     27.5     27.3     1.0     1.0       5.5     25.5     24.6     1.0     1.0       5.3     25.4     25.3     1.0     1.0       5.1     24.9     24.7     1.0     1.0       5.1     24.6     24.2     1.0     1.0       5.1     24.6     24.2     1.0     1.0       4.0     23.2     23.5     1.0     1.1	2.0       19.0       18.0       1.1       0.9         0.2       18.6       16.5       1.1       0.9         1.9       18.3       16.9       1.1       0.9         1.4       17.9       16.4       1.1       0.9         9.6       15.8       14.8       1.1       0.9         8.8       12.2       10.8       1.1       0.9         6.8       29.0       28.1       1.0       1.0         3.9       28.3       28.1       1.0       1.0         7.1       27.5       27.3       1.0       1.0         5.5       25.5       24.6       1.0       1.0         5.3       25.4       25.3       1.0       1.0         5.1       24.9       24.7       1.0       1.0         5.1       24.6       24.2       1.0       1.0         5.1       24.6       24.2       1.0       1.0         4.0       23.2       23.5       1.0       1.1	6.3 4.5 3.7 1.2 0.8 2.0 19.0 18.0 1.1 0.9 0.2 18.6 16.5 1.1 0.9 1.9 18.3 16.9 1.1 0.9 9.6 15.8 14.8 1.1 0.9 8.8 12.2 10.8 1.1 0.1 6.8 29.0 28.1 1.0 1.0 3.9 28.3 28.1 1.0 1.0 7.1 27.5 27.3 1.0 1.0 5.5 25.5 24.6 1.0 1.0 5.1 24.6 24.7 1.0 1.0 5.6 23.3 23.7 1.0 1.0 4.0 23.2 23.5 1.0 1.0	1.5     19.5     15.7     1.2     0.8       6.3     4.5     3.7     1.2     0.8       2.0     19.0     18.0     1.1     0.9       0.2     18.6     16.5     1.1     0.9       1.9     18.3     16.9     1.1     0.9       1.4     17.9     16.4     1.1     0.9       9.6     15.8     14.8     1.1     0.9       8.8     12.2     10.8     1.1     0.9       6.8     29.0     28.1     1.0     1.0       3.9     28.3     28.1     1.0     1.0       7.1     27.5     27.3     1.0     1.0       5.5     25.5     24.6     1.0     1.0       5.3     25.4     25.3     1.0     1.0       5.1     24.9     24.7     1.0     1.0       5.1     24.6     24.2     1.0     1.0       5.6     23.3     23.7     1.0     1.0       4.0     23.2     23.5     1.0     1.1	3.0     19.9     16.4     1.2     0.8       1.5     19.5     15.7     1.2     0.8       6.3     4.5     3.7     1.2     0.8       2.0     19.0     18.0     1.1     0.9       0.2     18.6     16.5     1.1     0.9       1.9     18.3     16.9     1.1     0.9       1.4     17.9     16.4     1.1     0.9       9.6     15.8     14.8     1.1     0.9       8.8     12.2     10.8     1.1     0.9       8.8     12.2     10.8     1.1     0.9       6.8     29.0     28.1     1.0     1.0       3.9     28.3     28.1     1.0     1.0       7.1     27.5     27.3     1.0     1.0       5.5     25.5     24.6     1.0     1.0       5.1     24.9     24.7     1.0     1.0       5.1     24.6     24.2     1.0     1.0       5.1     24.6     24.7     1.0     1.0       5.1     24.6     24.7     1.0     1.0       5.1     24.6     24.7     1.0     1.0       5.1     24.6     24.7     1.0     1.0	3.7     23.8     19.4     1.2     0.8       3.0     19.9     16.4     1.2     0.8       1.5     19.5     15.7     1.2     0.8       6.3     4.5     3.7     1.2     0.8       2.0     19.0     18.0     1.1     0.9       1.9     18.6     16.5     1.1     0.9       1.4     17.9     16.4     1.1     0.9       9.6     15.8     14.8     1.1     0.9       9.6     15.8     14.8     1.1     0.9       9.6     15.8     14.8     1.1     0.9       10.8     12.2     10.8     1.1     0.9       10.8     12.2     10.8     1.1     0.9       10.8     12.2     10.0     1.1     0.9       10.8     12.2     10.0     1.1     0.9       10.8     12.2     10.0     1.1     0.9       10.0     1.0     1.0     1.1       10.1     27.5     27.3     1.0     1.1       10.5     25.4     25.3     1.0     1.1       10.5     24.6     24.7     1.0     1.1       10.5     23.3     23.7     1.0     1.1	8.8       26.1       22.6       1.2       0.9         3.7       23.8       19.4       1.2       0.8         1.5       19.9       16.4       1.2       0.8         6.3       4.5       15.7       1.2       0.8         2.0       19.0       18.0       1.1       0.9         1.9       18.6       16.5       1.1       0.9         1.9       18.3       16.9       1.1       0.9         1.4       17.9       16.4       1.1       0.9         9.6       15.8       14.8       1.1       0.9         9.6       15.8       14.8       1.1       0.9         9.6       15.8       14.8       1.1       0.9         9.6       15.8       10.8       1.1       0.9         9.6       15.8       11.0       1.1       0.9         9.6       15.8       11.0       1.1       0.9         9.6       15.8       11.0       1.1       0.9         9.6       15.8       11.0       1.1       0.9         9.6       15.8       10.8       1.1       0.9         9.1       10.8       1.1 </td <td>2.4       21.0       16.5       1.3       0.8         8.8       26.1       22.6       1.2       0.9         3.7       23.8       19.4       1.2       0.8         3.0       19.9       16.4       1.2       0.8         6.3       4.5       15.7       1.2       0.8         6.3       4.5       3.7       1.2       0.8         2.0       19.0       18.0       1.1       0.9         2.0       19.0       18.0       1.1       0.9         1.9       18.6       16.5       1.1       0.9         1.9       18.3       16.9       1.1       0.9         1.4       17.9       16.4       1.1       0.9         1.4       17.9       16.4       1.1       0.9         1.0       1.2       10.8       1.1       0.9         1.0       1.0       1.1       0.9         1.0       1.0       1.0       1.0         1.0       28.1       1.0       1.0         2.1       27.5       27.3       1.0       1.0         2.1       24.6       1.0       1.0         2.1</td> <td>4.6       17.1       11.9       1.4       0.7         2.4       21.0       16.5       1.3       0.8         8.8       26.1       22.6       1.2       0.9         3.7       23.8       19.4       1.2       0.8         3.0       19.9       16.4       1.2       0.8         6.3       4.5       3.7       1.2       0.8         6.3       4.5       3.7       1.2       0.8         6.3       4.5       3.7       1.2       0.8         10.2       18.6       16.5       1.1       0.9         11.9       18.6       16.9       1.1       0.9         11.4       17.9       16.4       1.1       0.9         19.6       15.8       14.8       1.1       0.9         19.6       15.8       14.8       1.1       0.9         19.6       15.8       14.8       1.1       0.9         19.6       15.8       14.8       1.1       0.9         19.6       15.8       10.8       1.1       0.9         19.6       15.8       10.8       1.1       0.9         19.6       15.8</td> <td>7.3 19.6 13.0 1.5 0.3 4.6 17.1 11.9 1.4 0.3 2.4 21.0 16.5 1.3 0.8 8.8 26.1 22.6 1.2 0.8 3.7 23.8 19.4 1.2 0.8 19.5 19.5 15.7 1.2 0.8 19.5 19.5 15.7 1.2 0.8 19.6 18.6 16.5 1.1 0.9 18.6 16.5 1.1 0.9 18.8 17.9 16.4 1.1 0.9 18.8 17.9 16.4 1.1 0.9 18.8 12.2 10.8 1.1 0.1 0.9 18.8 12.2 10.8 1.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1</td> <td>2.9       18.6       11.8       1.6       0.6         7.3       19.6       13.0       1.5       0.7         4.6       17.1       11.9       1.4       0.7         2.4       21.0       16.5       1.3       0.8         2.4       21.0       16.5       1.2       0.8         3.7       23.8       19.4       1.2       0.8         3.7       12.2       0.8         6.3       4.5       3.7       1.2       0.8         6.3       4.5       3.7       1.2       0.8         1.0       19.0       18.0       1.1       0.9         1.0       19.0       18.0       1.1       0.9         1.0       1.2       0.8       1.1       0.9         1.0       1.2       0.8       1.1       0.9         1.0       1.2       0.8       1.1       0.9         1.0       1.3       16.4       1.1       0.9         1.0       1.8       1.1       0.9       1.1         1.0       1.3       1.0       1.1       0.9         1.0       1.1       0.9       1.1       0.9</td> <td>9.8       17.5       16.3       1.1       0.9         2.9       18.6       11.8       1.6       0.6         7.3       19.6       13.0       1.5       0.6         7.3       19.6       13.0       1.5       0.6         2.4       21.0       16.5       1.3       0.8         8.8       26.1       22.6       1.2       0.8         3.7       23.8       19.4       1.2       0.8         3.0       19.9       16.4       1.2       0.8         6.3       4.5       3.7       1.2       0.8         6.3       4.5       3.7       1.2       0.8         1.9       18.6       16.5       1.1       0.9         1.0       1.1       0.9       1.1       0.9         1.4       17.9       16.4       1.1       0.9         1.4       17.9       16.4       1.1       0.9         1.4       17.9       16.4       1.1       0.9         1.0       1.1       0.9       1.1       0.9         1.0       1.1       0.9       1.1       0.9         1.0       1.1       0.9</td> <td>9.8 17.5 16.3 1.1 0.9 2.9 18.6 11.8 1.6 0.6 7.3 19.6 13.0 1.5 0.7 4.6 17.1 11.9 1.4 0.7 2.4 21.0 16.5 1.3 0.8 8.8 26.1 22.6 1.2 0.8 3.7 23.8 19.4 1.2 0.8 1.5 19.5 15.7 1.2 0.8 6.3 4.5 3.7 1.2 0.8 1.4 17.9 16.4 1.1 0.8 1.4 17.9 16.4 1.1 0.8 9.6 15.8 14.8 1.1 0.8 9.6 15.8 14.8 1.1 0.8 9.6 15.8 29.0 28.1 1.0 0.8 8.8 12.2 10.8 1.1 0.8 9.6 29.3 28.1 1.0 1.1 9.6 15.8 29.0 28.1 1.0 1.1 9.6 15.8 29.0 28.1 1.0 1.1 9.6 15.8 29.0 28.1 1.0 1.1 9.6 15.8 29.0 28.1 1.0 1.1 9.6 15.8 29.0 28.1 1.0 1.1 9.6 1.0 1.0 1.0 1.0 1.0 2.1 27.5 27.3 1.0 1.0 2.1 27.5 23.3 25.4 25.3 1.0 1.0 1.0 1.0 2.1 27.5 23.3 23.7 1.0 1.0 1.0 1.0 2.1 23.2 23.5 1.0 1.0</td> <td>Fig IGFSR IR IGFR/IR IR/IGFF 19.8 17.5 16.3 1.1 0.9 2.9 18.6 11.8 1.6 0.6 7.3 19.6 13.0 1.5 0.7 4.6 17.1 11.9 1.4 0.7 3.7 23.8 19.4 1.2 0.8 3.7 23.8 19.4 1.2 0.8 6.3 4.5 3.7 1.2 0.8 6.3 19.9 16.4 1.2 0.8 6.3 19.9 16.4 1.2 0.8 6.3 19.0 18.0 1.1 0.9 11.4 17.9 16.4 1.1 0.9 11.4 17.9 16.4 1.1 0.9 11.4 17.9 16.4 1.1 0.9 11.4 17.9 16.4 1.1 0.9 11.4 17.9 28.1 1.0 0.9 18.8 12.2 10.8 1.1 0.9 18.8 12.2 10.8 1.1 0.9 18.8 29.0 28.1 1.0 1.1 18.5 25.5 24.6 1.0 1.0 18.5 25.5 24.6 1.0 1.0 18.6 23.3 23.7 1.0 1.0 18.6 23.3 23.7 1.0 1.0 18.6 23.3 23.7 1.0 1.0 18.6 23.3 23.7 1.0 1.0</td>	2.4       21.0       16.5       1.3       0.8         8.8       26.1       22.6       1.2       0.9         3.7       23.8       19.4       1.2       0.8         3.0       19.9       16.4       1.2       0.8         6.3       4.5       15.7       1.2       0.8         6.3       4.5       3.7       1.2       0.8         2.0       19.0       18.0       1.1       0.9         2.0       19.0       18.0       1.1       0.9         1.9       18.6       16.5       1.1       0.9         1.9       18.3       16.9       1.1       0.9         1.4       17.9       16.4       1.1       0.9         1.4       17.9       16.4       1.1       0.9         1.0       1.2       10.8       1.1       0.9         1.0       1.0       1.1       0.9         1.0       1.0       1.0       1.0         1.0       28.1       1.0       1.0         2.1       27.5       27.3       1.0       1.0         2.1       24.6       1.0       1.0         2.1	4.6       17.1       11.9       1.4       0.7         2.4       21.0       16.5       1.3       0.8         8.8       26.1       22.6       1.2       0.9         3.7       23.8       19.4       1.2       0.8         3.0       19.9       16.4       1.2       0.8         6.3       4.5       3.7       1.2       0.8         6.3       4.5       3.7       1.2       0.8         6.3       4.5       3.7       1.2       0.8         10.2       18.6       16.5       1.1       0.9         11.9       18.6       16.9       1.1       0.9         11.4       17.9       16.4       1.1       0.9         19.6       15.8       14.8       1.1       0.9         19.6       15.8       14.8       1.1       0.9         19.6       15.8       14.8       1.1       0.9         19.6       15.8       14.8       1.1       0.9         19.6       15.8       10.8       1.1       0.9         19.6       15.8       10.8       1.1       0.9         19.6       15.8	7.3 19.6 13.0 1.5 0.3 4.6 17.1 11.9 1.4 0.3 2.4 21.0 16.5 1.3 0.8 8.8 26.1 22.6 1.2 0.8 3.7 23.8 19.4 1.2 0.8 19.5 19.5 15.7 1.2 0.8 19.5 19.5 15.7 1.2 0.8 19.6 18.6 16.5 1.1 0.9 18.6 16.5 1.1 0.9 18.8 17.9 16.4 1.1 0.9 18.8 17.9 16.4 1.1 0.9 18.8 12.2 10.8 1.1 0.1 0.9 18.8 12.2 10.8 1.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1	2.9       18.6       11.8       1.6       0.6         7.3       19.6       13.0       1.5       0.7         4.6       17.1       11.9       1.4       0.7         2.4       21.0       16.5       1.3       0.8         2.4       21.0       16.5       1.2       0.8         3.7       23.8       19.4       1.2       0.8         3.7       12.2       0.8         6.3       4.5       3.7       1.2       0.8         6.3       4.5       3.7       1.2       0.8         1.0       19.0       18.0       1.1       0.9         1.0       19.0       18.0       1.1       0.9         1.0       1.2       0.8       1.1       0.9         1.0       1.2       0.8       1.1       0.9         1.0       1.2       0.8       1.1       0.9         1.0       1.3       16.4       1.1       0.9         1.0       1.8       1.1       0.9       1.1         1.0       1.3       1.0       1.1       0.9         1.0       1.1       0.9       1.1       0.9	9.8       17.5       16.3       1.1       0.9         2.9       18.6       11.8       1.6       0.6         7.3       19.6       13.0       1.5       0.6         7.3       19.6       13.0       1.5       0.6         2.4       21.0       16.5       1.3       0.8         8.8       26.1       22.6       1.2       0.8         3.7       23.8       19.4       1.2       0.8         3.0       19.9       16.4       1.2       0.8         6.3       4.5       3.7       1.2       0.8         6.3       4.5       3.7       1.2       0.8         1.9       18.6       16.5       1.1       0.9         1.0       1.1       0.9       1.1       0.9         1.4       17.9       16.4       1.1       0.9         1.4       17.9       16.4       1.1       0.9         1.4       17.9       16.4       1.1       0.9         1.0       1.1       0.9       1.1       0.9         1.0       1.1       0.9       1.1       0.9         1.0       1.1       0.9	9.8 17.5 16.3 1.1 0.9 2.9 18.6 11.8 1.6 0.6 7.3 19.6 13.0 1.5 0.7 4.6 17.1 11.9 1.4 0.7 2.4 21.0 16.5 1.3 0.8 8.8 26.1 22.6 1.2 0.8 3.7 23.8 19.4 1.2 0.8 1.5 19.5 15.7 1.2 0.8 6.3 4.5 3.7 1.2 0.8 1.4 17.9 16.4 1.1 0.8 1.4 17.9 16.4 1.1 0.8 9.6 15.8 14.8 1.1 0.8 9.6 15.8 14.8 1.1 0.8 9.6 15.8 29.0 28.1 1.0 0.8 8.8 12.2 10.8 1.1 0.8 9.6 29.3 28.1 1.0 1.1 9.6 15.8 29.0 28.1 1.0 1.1 9.6 15.8 29.0 28.1 1.0 1.1 9.6 15.8 29.0 28.1 1.0 1.1 9.6 15.8 29.0 28.1 1.0 1.1 9.6 15.8 29.0 28.1 1.0 1.1 9.6 1.0 1.0 1.0 1.0 1.0 2.1 27.5 27.3 1.0 1.0 2.1 27.5 23.3 25.4 25.3 1.0 1.0 1.0 1.0 2.1 27.5 23.3 23.7 1.0 1.0 1.0 1.0 2.1 23.2 23.5 1.0 1.0	Fig IGFSR IR IGFR/IR IR/IGFF 19.8 17.5 16.3 1.1 0.9 2.9 18.6 11.8 1.6 0.6 7.3 19.6 13.0 1.5 0.7 4.6 17.1 11.9 1.4 0.7 3.7 23.8 19.4 1.2 0.8 3.7 23.8 19.4 1.2 0.8 6.3 4.5 3.7 1.2 0.8 6.3 19.9 16.4 1.2 0.8 6.3 19.9 16.4 1.2 0.8 6.3 19.0 18.0 1.1 0.9 11.4 17.9 16.4 1.1 0.9 11.4 17.9 16.4 1.1 0.9 11.4 17.9 16.4 1.1 0.9 11.4 17.9 16.4 1.1 0.9 11.4 17.9 28.1 1.0 0.9 18.8 12.2 10.8 1.1 0.9 18.8 12.2 10.8 1.1 0.9 18.8 29.0 28.1 1.0 1.1 18.5 25.5 24.6 1.0 1.0 18.5 25.5 24.6 1.0 1.0 18.6 23.3 23.7 1.0 1.0 18.6 23.3 23.7 1.0 1.0 18.6 23.3 23.7 1.0 1.0 18.6 23.3 23.7 1.0 1.0



RRSDSSLHRSFYDWFSVQLLN	(
I GAUGULHAKE TAWE BEQUKE	CローコーロコーT
	H2CB-3-C3-IGFR
TSEVGDFHAEFYSWFEIQLGR	H2CB-3-D9-IGFR
SLVAADLHEGFYGWFRSQLGG	H2CB-4-G4-IGFR
WGEGGGFYDWFYDQLGWEPSH	H2CB-3-B5-IGFR
ERETAAFGQAFYQWFRDQIAG	H2CB-3-C4-IGFR
RDTLPAFHQHFYQWFEKQVSA	H2CB-3-A10-IGFR
GNFREAFHADFYSWFERQLQS	H2CB-4-H2-IGFR
RRGRDGFHGGFYDWFAAQLSD	H2CB-4-E9-IGFR
HTGAGDLHGAFYNWFLEQLGG	H2CB-4-G6-IGFR
<b>ASHKSAFDDNFYRWFSMQLRD</b>	H2CB-4-E7-IGFR
LDEDLPQHAGFYGWFAEALGV	H2CB-3-B4-IGFR
TAAISDFNSLFYGWFEQLLSS	H2CB-3-A3-IGFR
GLAPGNFHEDFYRWFQEQTLG	H2CB-3-A9-IGFR
RPASRPFHSGFYQWFADQLSH	H2CB-3-B12-IGFR
MGGATFFHTGFYDWFAAQLQH	H2CB-3-A12-IGFR
SRVSDPYHVGFYQWFEEVVRG	H2CB-3-C8-IGFR
GLQNVSFHSGFYEWFARQVSQ	H2CB-4-G9-IGFR
WAGGSDVDGSFYDWFQRLLAS	H2CB-3-D12-IGFR
FRHITEVDRSFYGWFVEQLRG	H2CB-4-E8-IGFR
SVFMQHDHVGFYAWFRSLMEE	H2CB-4-E5-IGFR
GYREMRSDLGFYQWFRDQLGL	H2CB-4-E4-IGFR
SGVFNGTFYDWFRIQLGE	H2CB-3-D8-IGFR
DSLGISFHEGFYDWFRRQLDM	H2CB-4-F4-IGFR
CSGLQRCHDSFYSWFESVVRE	H2CB-4-G7-IGFR
KVDLRGFHDGFYGWFARQLAG	H2CB-4-H5-IGFR
GALSSLFDAAFYDWFNRQLEG	H2CB-4-H10-IGFR
XXXXXXFHXXFYXWFXXXXXX	<b>Design</b>
Sequence	Clone

E-Tag 21.9 22.3 23.1 21.6 22.0 21.6 22.0 21.6 22.0 21.6 22.0	ios over Backgro ing IGESR 1.9 22.4 2.3 22.3 3.1 21.6 1.3 20.9 2.0 20.5 1.6 20.5 1.6 20.5 1.6 20.5 1.6 19.7 1.1 19.7 1.1 19.7 1.6 17.3 1.6 14.5	23.3 23.6 21.6 20.6 21.3 21.3 21.6 21.3 21.3 21.3 21.3	Compan IGFRVIR 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0	risons 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0
0.			1.0	
1			1.0	_
	•	•	1.0	_
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<u>ი</u>			1.0	_
		5	1.0	_
0	ω ·	W	1.0	_
8	7.	9	0.9	_
7.	5	7.	0.9	
7.		25.7	0.9	_
<u>ه</u> .	24.1	6	0.9	
5	u.	5	0.9	
4.	-	4	0.9	
2	1	ω ·	0.9	
4.		2.	0.9	
ب		-	0.9	
4.		۲.	0.9	
w •	19.2	22.0	0.9	
4.		0	0.9	
1		۲.	0.9	
4		•	0.9	
	18.4	21.1	0.9	
2	8	•	0.9	
œ •		œ		

Figure 1N (Con't)



H2CB-4-F12-IGFR	H2CB-4-G5-IGFR	H2CB-3-A11-IGFR	H2CB-4-G2-IGFR	H2CB-3-C1-IGFR	H2CB-4-E3-IGFR	H2CB-3-C10-IGFR	H2CB-3-D7-IGFR	H2CB-3-D11-IGFR	H2CB-4-G1-IGFR	H2CB-4-F5-IGFR	H2CB-4-H7-IGFR	H2CB-3-C7-IGFR	H2CB-3-B8-IGFR	H2CB-4-F6-IGFR	H2CB-3-C5-IGFR	H2CB-3-B1-IGFR	H2CB-3-A4-IGFR	H2CB-4-F3-IGFR	H2CB-3-D6-IGFR	H2CB-4-E11-IGFR	H2CB-3-C6-IGFR	H2CB-4-F1-IGFR	H2CB-3-A8-IGFR	H2CB-4-F8-IGFR	H2CB-4-E10-IGFR	H2CB-4-F9-IGFR	H2CB-4-H1-IGFR	Design	Clone
DORMGSFHGEFYRWFEETLLS	QRSAVEFHADFYDWFLRLLTP	LDKGWGFDL <u>Q</u> FYRWFEAATRA	GSGLYVFHWGFYDWFEQQMGG	GANALGEKDREYEWFAAQLWD	MWLWATLHSDFYSWFEQVVSG	YLQRAGFHRSFYGWFDQALRD	QQSAGHPHSSFYLWFSELLGA	EGFGVLFHGQFYRWFQLQLDG	SGTAADLHSRFYGWFALQARE	EHTSYQIHRQFYEWFDRALGR	<b>GAFGSEFHE<u>Ö</u>FYRWFEDALSF</b>	FQCGAAFHVDFYRWFTCQEQF	QSPYGFFHDGFYRWFLQQTGM	VRSEQRFDSSFYQWFNDLLMS	GREIGGVHDGFYDWFRQQSEQ	RLAGSGIHEGFYGWFVDQLLA	<b>QLGMDWFHADFYEWFLAQLPS</b>	AAVNSLFHDEFYLWFQDQLDG	GRSVSRMNAEFYQWFGHQLAA	<b>QAGGMEFHGAFYNWFLQQLSG</b>	FDAVHGFDGGFYGWFKRELQR	AVHAATFHDDFYRWFEQVVGS	WAPPDALHGQFYRWFQRQLDQ	MRTAELFHVGFYDWFDAQLMD	<u>LQRYIGFHDPFYDWFSRALSG</u>	LINA.VFRRGFYAWFEEQVSK	HGVIRADHTGFYGWFSKQLSD	XXXXXXFHXXFYXWFXXXXXX	Sequence

	Ratios ov	er Backgro	round	Compa	risons	
	Ę-Tag IÇFsR	ICFSR	₹	ICFR/IR	GFR/IR IR/IGFR	
	:	;	;	;	:	
,	•	15.3	16.5	0.9	1.1	
	22.9	14.4	•	0.9	1.1	
	•	20.1		0.8	1.2	
	21.5	14.8	•	0.8	1.3	
	0	14.7	18.2	0.8	1.2	
	22.2	•	18.8	0.8	1.3	
	15.7	٠		0.8	1.3	
	6	•	•	0.7	1.4	
	21.6	•	18.8	0.7	1.5	
	17.3	11.1	16.4	0.7	1.5	
	27.4	•	14.8	0.7	1.3	
	20.0	•	•	0.7	1.4	
	9	10.5	•	0.7	1.5	
	18.6	10.1		0.7	1.4	
	Ö	6.9		0.7	1.4	
	16.2	1.8		0.7	1.4	
	_	14.1	22.7	0.6	1.6	
	2	4.0		0.6	1.8	
	20.4	10.3		0.5	1.9	
	24.1	8.8	•	0.5	2.1	
	2	6.5		0.5	2.1	
	1.	5.1		0.5	2.0	
	20.3	4.6	8.9	0.5	1.9	
	•	6.7		0.4	2.3	
	19.9	ω . ω	10.7	0.3	ພ ພ	
		•	•	0.3	3.1	
	9.			0.3	3.1	
	ע					



20E2Bα-4-G12-IR 20E2Bα-3-C11-IR 20E2Bα-3-C10-IR	20E2Bβ-3-E11-IR 20E2Bα-3-B11-IR NNKH-4-G2-IR	20E2Bα-3-C12-IR 20E2Bβ-3-C12-IR 20E2Bβ-3-E7-IR	20E2Bβ-4-F9-IR 20E2Bβ-3-E9-IR 20E2Bβ-3-E10-IR	20E2Bu-4-H9-IR 20E2Bu-3-B1-IR	20E2B }-3-E3-IR rB6-3-F6-IR rB6-4-F9-IR	Clone Design 20E2A-3-B11-IR
MQGHRGFYGWFARVLEQDRGW ERLHLRFYEWFDTVIGQDGSD MHVQSDFYHWFQSLLGQGGPD	TLIQDQFYWWFSDLLSAEFGD IDQLDAFYRWFDGVMLGMGDP RGGGTFYEWFESALRKHGAG	SSQDRRFYRWFEQAIVGGRDG TRGQLGFYNWFQQALSTSGMG CADLNAFYQWFCGVLDRGSDH	QSPRASFYGWFDDVLRAAGVV TGFYEWFYEQLHSRMLPNPLD RRGVGGFYGWFSQQLQGMGVA	PYRMEGTEKWNFYDWFVAQLQ SAVHFQFYKWFDNLLPVPLSA VPVNKSFYRWFQLVLGGSDDW	IQGWEPFYGWFDDVVAQMFEE RYGRWGLAQQFYDWFDR RGRLGSLSTQFYNWFAE ASAYTPFYOWFADVVSEYMQQ	Sequence X <sub>n</sub> -FyxWF-X <sub>m</sub> GRFYGWFQDAIDQLMPWGFDP

	37.7	37.3	37.0	19.0	10.8	36.0	20.7	9.2	20.2	39.0	22.2	27.0	25.9	41.8	37.8	28.9	35.4	34.1	40.9	23.0	24.6	1	Ratios ove Ę-Tag
1	24.8	26.8	22.3	4.2	6.3	20.7	1.3	1.2	2.2	6.7	2.6	7.7	4.2	12.9	9.4	4.1	7.4	1.0	1.0	0.9	1.4	:	er Backgro IGFsR
	30.5	34.8	29.5	5.5	8.9	32.8	2.1	1.9	3.8	12.0	5.5	17.2	10.1	36.8	26.7	18.1	34.4	12.6	13.3	15.3	23.6	1	und IR
	0.8	0.8	0.8	0.8	0.7	0.6	0.6	0.6	0.6	0.6	0.5	0.5	0.4	0.4	0.4	0.2	0.2	0.1	0.1	0.1	0.1	:	Compai IGFR/IR
	1.2	1.3	1.3	1.3	1.4	1.6	1.6	1.6	1.8	1.8	2.1	2.2	2.4	2.9	2.9	4.4	4.6	12.6	13.3	16.3	16.8	1	isons IIVIÇFR



20E2Bu-4-H6-IR	20E2Ba-4-G2-IR	20E2Bα-3-B2-IR	20E2Bα-3-C2-IR	A6L-4-F11-IR	20E2Bu-3-B9-IR	20E2Bα-3-C5-IR	20E2Bα-3-C7-IR	20E2Bα-3-B10-IR	20E2Bα-4-G5-IR	20E2Bu-4-F8-IR	20E2Bu-4-G4-IR	20E2Bα-4-F6-IR	20E2Bα-4-H10-IR	20E2Bα-4-E8-IR	20E2Bμ-4-E11-IR	20E2Bu-4-E12-IR	20E2Bu-3-A4-IR	20E2Bu-3-C9-IR	20E2Bα-4-F5-IR	20E2Bu-4-G7-IR	20E2Bu-3-D10-IR	20E2Bu-3-A12-IR	20E2Bα-3-D7-IR	Design	Clone
SHLTDPFYQWFVDQLRAGVRG	GVVEGTFYEWFDRLLGGVQGD	ARRADGFYDWFREQVSGSAVQ	<b>VPNSWMFYNWFAEQIEGSEGE</b>	LLGLS <u>Q</u> AAYANFYDWFVS <u>Q</u> LA	SNGISGFYEWFAAQVQTSDFQ	PAVGQSFYGWFEAVLRGSKAG	GVLSTGFYEWFALQLHGLAAG	RLLLGGFYEWFDQVLKETKEV	GRQDREFYYWFELQAGGMDGD	TVDHTQFYDWFSRVLGESGSA	RGTDDTFYGWFDQLLQGWCDD	<b>DNMSGGFYRWFAQVVADSGGD</b>	QGVEGGFYEWFDRAMGDVRPW	SGTPYGFYRWFQSALASATSG	ASGFDPFYAWFLEQLRVANGS	MQRNQGFYSWFDDLVSSTVGV	QSPRASFYGWFDDVLRAAGVV	ANLNSQFYSWFASVTGEASPS	GIRSSGFYQWFDRVLAGVGDG	MQLQDEFYNWFRGIMLNDGQD	VRRDAGFYQWFADILTQLDFE	ITHNRGFYSWFLDVVQGGAGA	TMGTQGFYRWFQNVVKEHLSG	Xn-FyxWF-Xm	Sequence

39.4	34.1	43.1	44.1	33.1	39.6	40.4	37.6	38.2	34.9	37.7	34.1	34.9	38.9	36.1	35.1	36.0	38.2	39.4	33.8	34.2	32.7	31.7	35.4	1	Ratios ov E-Tag
36.0	33.6	40.1	40.0	4.6	35.8	36.0	34.2	34.9	33.9	32.0	33.7	33.2	30.6	30.5	31.2	30.8	31.6	33.2	32.1	29.0	27.3	. 22.0	26.9	1	Ratios over Backgro E-Tag IGFsR
31.9	29.8	39.0	38.1	4.6	37.1	35.6	34.8	33.6	33.4	32.7	32.2	32.0	30.7	30.7	30.7	29.7	35.9	35.5	34.0	30.7	29.1	23.3	31.3	1	round IR
1.1	1.1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.9	0.9	0.9	0.9	0.9	0.9	0.9	;	Compari IGFR/IR
0.9	0.9	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.φ	1.0	1.0	1.0	1.0	1.0	1.1	1.1	1.1	1.1	1.1	1.1	1.2	;	risons IR/IGFR

Figure 10 (Con't)



20Ε2Ββ-4-H10-IR rB6-4-G8-IR	20E2Bβ-4-G6-IR	H5-3-D5-IR	20E2Bα-4-E6-IR	20E2Bu-3-C1-IR	20E2Bα-4-H4-IR	20ξ2Bα-4-G3-IR	20E2Ba-4-H5-IR	Design	Clone
SNGISGFYEWFAAQVQTSDFQ RRDRGGLDVFFYQWFMD	SQAGSAFYAWFDQVLRTVHSA	IVVPGDTQGVNFYDWFVKQLQ RDVSMGSASTNFYDWFVOOLG	CGQTQSFYQWFCEVMRVESGD	SLGQGGFYDWFASQVGGADI	PGLHRAFYQWFAEAVRSANKE	DSDGAQFYIWFEDQLRSAGWD	RSNDDAFYRWFSNILQVDGGG	Xn-FyxWF-Xm	Sequence

Ratios ov E-Tag	Ratios over Backgrot E-Tag IGFsR	IR IR	Compai IGFR/IR	risons IR/IGFR 
38.7	35.1	32.3	1.1	0.9
35.5	36.1	32.7	1.1	<b>0</b> .9
38.8	37.9	35.0	1.1	0.9
43.7	42.1	39.0	1.1	0.9
38.0	34.3	29.7	1.2	0.9
43.8	21.8	18.2	1.2	0.8
38.3	29.8	25.3	1.2	0.8
22.4	6.2	1.9	ω . ω	0.3
23.5	32.2	9.7	3.3	0.3

Figure 1O (Con't)

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Clone Design R40-3-40H4-IR

FIGURE 2A



				i	)	•
		Ratios ov	Ratios over Background	pur	Comparisons	isons
Clone	Sequence	E-Tag	IGFsR IR	Ħ	IGEWIR INIGH	RIGHR
Design	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	!		;		!
R40-3-B6-IGFR	AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA	1		:		1
R40-X-E5-IGFR	RHLTNÄELGVQSPEVLSRLFPDGDIFYRALSHLVRGMGPP	!		. [		1
R40-X-B5-IGFR	RGGMDRQWLDVGARHRLERRSVQDNTDDFYGGLRILVDGF	1		!		:
R40-4-9-IGFR	GPPDSFDVTEKGDMAILNVRFDPHSLDFNDQTFYFLLDSL	i i		1	1	•
R40-3-G6-IGFR	GGTYFRGQVAQSNESLLRVNFLQLLEALAASPPRT	;	1	1		;
R40-4-12-IGFR	APFDARLSAPRFQWSPRTWXQSLSYGEWSCGSFYDCLSSI	ŧ	!	•		i t
R40-3-A5-IGFR	MGSSQFQDTRPSSGQAYSHSLDSDGWGTANWIFLRALEGL	i i	;	1	1	:
R40-X-C6-IGFR	SGAAHEGNQGRERSTHLAANINDHLPGDAGIWLGYSWLS		:	:	1	:



R20β-4-A6-IR	R20β-4-C6-IR	R2Qα-4-20A12-IR	R20u-3-20E2-IR	R20α-4-20C11-IR	Clone Design
RGQSDAFYSGLWALIGLSDG	FYSALWGLCGVTGCG	IR RLFYCGIQALGANLGYSGCV	R FYDAIDQLVRGSARAGGTRD	IR DRAFYNGLRDLVGAVYGAWD	Sequence XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

Ratios ov	er Backgro	ψnφ	Comparisons	risons	
E-Tag	E-Tag IGFsR IR	R	IGFIVIR IN/IGFR	IR/IGFR	
:	!	!	;	1	
43.7	30.8	3.0	10.3	0.1	
46.3	39.9	3.1	12.9	0.1	
48.6	39.9	2.4	16.6	0.1	
18.5	28.9	4.3	6.7	0.1	
,	י ר	_	ני	0.1	



Clone  pesign  R20-4-F11-IGFR  R20-4-C7-IGFR  R20-3-F2-IGFR	Sequence XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
R20-4-A11-IGFR R20-4-B12-IGFR	PFYVWIRDLLGPELPHTRGD VLVVGGPLDPFYEGLHRLIS
R20-4-B10-IGFR	GFYRLLNELVREGGALKVGA
	DWVSGPFYRGIELLSGFQIE
R20-3-G2-IGFR	GGSLFYEGLLRLVLGDSVVG
R20-4-B8-IGFR	LNHFYAMLSDLSGVRNIFPG
R20-4-E7-IGFR	LSGFYEGLFRLARRDGSGWG
R20-4-G9-IGFR	FYDVLSALVGVELGEQGDAS
R20-4-D9-IGFR	GAGSFGREGGFYEALMQLAG
R20-4-D11-IGFR	DDEFYSQILKLVDGSRGGRSGTQN
R20-4-G10-IGFR	PFYMLLSRLVGGVEQEGGL
R20-4-C8-IGFR	FYDAIDQLVRGSARAGGTRD

										٠								
16.8	13.6	31.3	23.4	25.0	35.4	32.8	20.8	30.3	34.2	37.0	37.2	37.8	31.8	33.4	39.0	:	E-Tag	Ratios ov
3.2	υ. <b>3</b>	4.0	6.3	6.4	6.4	6.5	6.9	7.8	9.4	9.5	10.0	13.5	14.3	17.5	19.2	•	<b>ICFsR</b>	tatios over Background
:	!	:	;	:	;	1	:	:	;	1	;	,	1	1	!	:	₹	und
!	!	1	1	!	1	1	:	1	-	1	1	t i	1	;	!	:	IGFIVIR	Comparisons
!	1	1	1	;	-	1	1 1	1	:	!	!	1	;	1	1	1	IR/IGER	risons



Clone	Sequence
<b>р</b> евідп	XXXXCXXXXXXXXXXXXXXXXXXXX
20C-3-G3-IGFR	TFYSCLASLLTGTPQPNRGPWERCR
20C-4-C7-IGFR	FFYDCLAALLQGVARYHDLCAVEIT
20C-3-F6-IGFR	QRDFCRFYERLTALVGGQVDGGWPC
20C-3-A1-IGFR	SSYGCDGFYLMLFSLGLVASQELEC
20C-3-A4-IGFR	QFYGCLLDLSLGVPSFGWRRRCITA
20C-3-E4-IGFR	FFYRCLSRLLGGQLGSRLGLSCIGD
20C-4-D11-IGFR	DLFYCMMMQLATAGVGGSLGGPVCG
20C-4-F7-IGFR	CDFYCALSRLSGQPRDRMPNYPGTS
20C-3-B2-IGFR	GSACDGFYACLHALVQGPGEW

Ratios ove	Ratios over Background E-Tag IGFsR H	und IR	Comparisons IGFR/IR IR/IC	risons IR/IGFR	
33.1	32.3	1.2	27.0	<0.1	
35.3	28.0	1.3	21.8	<0.1	
33.5	26.1	1.9	14.1	0.1	
26.5	20.8	1.5	13.7	0.1	
17.7	8.8	1.2	7.6	0.1	
37.7	7.7	1.3	6.0	0.2	
33.3	17.2	6.1	2.8	0.4	
31.2	28.9	17.0	1.7	0.6	
37.7	35.2	30.9	1.1	0.9	



				i
Clone	Sequence	Ratios ov	ver Background IGFsR 11	R und
Parental/Design	AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA	;	1	:
B6L-4-C8-IR	ANLRLR?VGNRL*SVWPGEQWNTVDP?YQKLYELVRESGA	40.5	6.1	40.
B6L-4-B7-IR	<b>AETPAQVGWNRLWSVWPGEHWNIVDPFYHKLSELLRESGD</b>	19.6	4.0	23.
B6L-3-H1-IR	AETPAHVC*TVGGLFGRVNTWNTVDPFYAKLSELLRESGA	20.6	2.8	2
В6Ļ-4-E12-IR	GQNSGSAWDGISLWSVWPGDVWNPVDPFYHKLSELLRESGA	15.5	4.1	ω
₿6Ļ-4-₽8-IR	AĒAPAQVGWNLLQPGEHWITVDPFYNKLSEĻLRESGA	36.0	9.4	<b>&amp;</b>
B6Ļ-4-F7-IR	AETPAQVGWNGLWSVWPGEH*NTVDPFYHKLSELLRESDG	37.8	24.6	20.
B6L-4-B11-IR	AETPAQVGQNGLWSVWPGEHWNTVDPFYQKLFELLRESGA	5.5	2.0	-
B6L-4-B12-IR	AETPAQVGQNRLWSVWPGELWNTVDPFYHKLSELLRESGA	6.8	2.0	_
B6L-4-B8-IR	T*QGETPAQVSLWPGEHWNTVDPFYHRLSELLRESGA	36.4	18.7	14.
B6L-4-E8-IR	QGETPAQIGWNPLWSGWPGEHWNTLDPFYRKLSELLRESGA	35.6	11.4	<b>&amp;</b>
B6L-3-G6-IR	VDTPAQVGWNRLWSVGPGEHWYTDDPFYH*LSELLRESGA	7.6	2.5	<u>_</u>
B6L-3-G5-IR	AETSAQVGWQRLWSVWPGDHWSTLDPFYHKLSELLRESGA	11.5	2.0	<b></b>
В6Ļ-4-E10-IR	*NSPRVGWNGLWSVWPGEHWNTWDPFYNKLSELLRESGV	14.8	3.2	2
B6L-4-F10-IR	<b>AETPAQIGWNRLQSVWPGEYWNTVDPFYLKLSELLRESSP</b>	26.2	11.5	7
B6L-3-F3-IR	ADTPAQVSGNRLQSVWRGDPWNTVDPFYHKLSELLRESGA	36.0	17.1	10
B6L-4-A7-IR	AGTPAQVG*NRLWSVWPGEHWNTVDPFYNKLSELLRESGA	11.6	3.4	_
B6L-4-G8-IR	D*QAWSVWPGQHWNTIDPFYHKLSELLRESGA	30.4	11.2	ഗ
B6L-4-F8-IR	AETLARVGWNRMQSVWPGEHWNTVDPFYHKLSELLRESGA	35.6	12.8	7
B6L-4-G7-IR	<b>AATRPQVGWNRVWSVQPGEHWNTVDPFYHKLSELLRESGS</b>	33.5	12.9	6
B6L-3-F4-IR	LTTPAQVGWNRLQSVWPGEHWNSVDPFYHKLSELLGESGA	16.9	6.3	2
B6L-3-H4-IR	ADNPAQVGWNRLWSVWPVEH*NTVDPFYHKLSELLRESGA	20.6	4.9	2
B6L-3-A6-IR	AETPAQVGWNRLQSDWPGGHWNTLDPFYHKLSELLRESGA	22.4	6.3	w
B6L-4-D7-IR	AETSVQVGWIRLQSVWPGEHWNTVDPFYHKLSELLRGSGA	14.3	4.8	<b>~</b>
B6L-3-E2-IR	G*NSAHVGWNRLWSFWPGEHWNTVDPFYEKLSELLRVSGG	29.2	16.7	ω

Comparisons IGFR/IR IR/IGFR

FIGURE 2F



	•
Sequence	-
<b>AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA</b>	
AETPAQVGGDRLWSVWPGEHWNTVDPFYHKLS?LLRESGA	
AE?PAQVGWNRLWSVWPGE?WNTVDPFYLKLSELL?ESGA	
AET?AQVGWNG?WSVWPGEHWNTVDPFYYKLSELLRESGA	
AETPAQVQWNRLWSVWPKDHWNTVDPFYHKLSELLRESGA	
<b>AETRAQVGSNRVWSVWPGEHWNTVDPFYHKLSELLRESGA</b>	
AETPAQVGWNRLWSVQPGSDWNTVDPFYHKLSELLRESGA	
DETSAQVGWNRLWSDWPGEQWNTLDPFYHKLSELLRESGA	
GETPAQVGWNRLWSVWPAEHWSTVDPFYHKLSELLRESGA	
<b>AETAAQVGWNRLQSVWPGEHWNSVDPFYHKLSELLRESGA</b>	
<b>AEAPDQVGQNRLWSVWPGEHWNTVDPFYDKLSELLRESGA</b>	
PETPAQVGGNRLQSGWPGEHWNTVDPFYHKLSELLRESGA	
AQTPAQVGWNYRLSSVWPGEHWNTVDPFYHKLSELLRESGA	
AETPAQVGWNRLWSVQPGEHWNTVDPFYHKLSELLRQSDA	
AETPAQVGWNRLWSVWPGEH*NTVDPFYHKLSELLRESGA	
AETPAQVGWNSLQSVWPGEHWNT?DPFYHKLSELLRESGA	
<b>AESPAQVGSNRLQSVWSGEHWNTVDPFYHKLSELLRESGA</b>	
<b>AETPAQVGQYRLSSVWPGEHGNTVDPFYHKLSELLRESGA</b>	
AETPAQVGWNRLWSVWPGEHWNTIDPFY*KLSELLRESGA	
<b>DETPAHVGWNRPQSAWFGERWNTVDPFYHKLSELLRESGA</b>	
AGTPAQVGWNRLRSVQPDEHWNTVDPFYHKLSELLRESGA	
AETPAQVGWQRLWSVWPGEHWNP?DPFYRKLSELLRESGA	
<b>AETPAQVGWNRLQSVWPGEHWNTVDPFYHKLSELLRESGA</b>	
<b>AETPAQVGWNRLWSVQPGEHWNTVDPFYHKLSELLRESGA</b>	
<b>AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA</b>	
	AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGGDRÍWSVWPGEHWNTVDPFYHKLS?LLRESGA AETPAQVGWNRLWSVWPGEHWNTVDPFYYKLSELLRESGA AETPAQVGWNRLWSVWPGEHWNTVDPFYYKLSELLRESGA AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLRSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLRSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLRSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLRSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA

														D									-	-		
Ratios ov	E-Tag	1	7.3	5.5	ъ. Ф	6.7	6.5	5.9	6.3	5.2	5.4	4.4	3.0	4.7	10.9	2.9	5	2.4	4.2	2.5	2.4	2.1	2.7	1.9	1.8	1.2
Ratios over Backgro	IGFsR	1	22.1	21.8	18.1	17.4	15.9	15.2	14.8	14.8	11.9	11.1	10.4	10.3	9.7	9.1	8.8	8.0	7.5	7.4	6.8	6.4	5.9	3.9	3.6	2.5
und .	IR	;	;	;	:		!	:		!	1	:	:	:	1	:	:	1		•	:		:	:	;	:
Comparisons	<b>IÇFIVIR</b>	;	!	!	!	;	!	1	:	:	:	!	:	!	1	!	:	1	!	!	!	1	1	! !	:	!
risons	HVIGER	:	!	1	:	:	;	;	;	!	;	1	;	!	1	1	;	1	1		:	•		!	;	;



Clone	Sequence
Design	OOUUUUUUJJJJDPFYHKLSELXXOO
B6Hu-3-F5-IR	GGAVAAAVVGSRADPFYHKLSELVQGS
B6Hu-2-D10-IR	SGGGQQRKAIATSDDPFYHKLSELLLGG
B6Hα-3-F1-IR	CSMAAVAEAGDDDDPFYHKLSELCQGS
B6Hα-3-E6-IR	CGAKMTGTPNDPFYHKLSELLQRG
B6Hα-1-B8-IR	CCVEAEEAVGRRGDPFYHKLSELTGCC
B6Hα-2-D5-IR	SRVVTMVIKRGSPDPFYHKLSELVQGR
B6Hα-1-B3-IR	GCITAENGAGDPFYHKLSELGGCS
B6Ha-3-E5-IR	RCGDEEGWQENRRDDPFYHKLSELFGGC
B6Hα-4-H9-IR	GCEVIAAEGRRDDPFYHKLSELCQGG
B6Hα-2-D8-IR	SSETAKMVTGTRDDPFYHKLSELVQGS
B6Hα-3-E4-IR	WLCDGGWKQRRPPGDPFYHKLSELIDCG
B6Hα-3-F7-IR	SRVAATKEKRPSDDPFYHKLSELLQGS
B6Hα-1-A3-IR	SRAKVEAEMPDSGDPFYHKLSELLASG
₿6Hα-4-H10-IR	GGAAKKTVVGSPDDPFYHKLSELLQGS
B6Hα-3-F6-IR	CGVGEQMEVTDDGDDPFYHKLSELLWSC
B6Hα-3-F3-IR	SGEQTATIEGPSNDPFYHKLSELIWGS
B6Hα-4-G8-IR	GGTKAVAKVGTRDDPFYHKLSELLQGS
B6Hα-2-D1-IR	GCEVIVEEGDSADPFYHKLSELCQGS
B6Hα-3-E7-IR	GCAVVEEAERSRGDPFYHKLSELIQGC
B6Hα-2-D6-IR	GRTMAVMAAGGPDDPFYHKLSELVQGG
B6Hα-3-F10-IR	GCVVEWQKWHGASDPFYHKLSELGGCS
B6Hα-3-E8-IR	RGKTAAVIVGRPADPFYHKLSELLQGG
B6Hα-2-C10-IR	SGAKVIVVTGDSGDPFYHKLSELLQGS
B6Hα-2-C7-IR	RGIVAMVEATEVGSDHDPFYHKLSELVQGS

45.1	46.9	47.6	47.2	33.5	47.0	11.7	32.3	18.1	48.9	50.5	37.4	41.5	43.1	19.3	17.4	28.8	33.1	39.6	44.6	18.2	22.5	20.8	42.7	1	Ratios ov E-Tag
6.7	5.8	5.3	8.8	4.4	5.6	5.4	6.1	15.6	19.7	29.5	2.6	3.1	8.7	3.0	6.4	2.9	3.2	2.3	5.2	2.3	2.4	1.7	9.6	!	Ratios over Background E-Tag IÇFsR II
1.0	1.1	1.1	1.9	1.0	1.3	1.3	1.7	4.3	5.7	8.6	0.8	1.0	2.8	1.0	2.1	1.0	1.1	0.9	2.1	1.2	1.3	1.1	17.9	;	ound IR
6.7	5.3	4.8	4.6	4.4	4.3	4.2	3.6	3.6	3.5	3.4	3.3	3.1	3.1	3.0		2.9		2.6	2.5	1.9	1.8	1.5	0.5	1	Compa IGFR/IR
0.1			0.2			0.2		0.3	0.3	0.3	0.3	0.3	Q.3	0.3	0.3	0.3		0.4	0.4			0.6	1.9	1	Comparisons GFR/IR IR/IGFR

FIGURE 2H



B6Hβ-3-C6-IR	B6Hβ-3-C9-IR	в6нβ-3-D3-IR	В6Hβ-3-H3-IR	86Hβ-3-A1-IR	B6Hβ-3-F5-IR	В6Hβ-3-G11-IR	в6нβ-3-в3-IR	B6Hβ-3-G1-IR	B6Hβ-3-A3-IR	B6Hβ-3-D9-IR	В6Hβ-3-A10-IR	B6Hβ-3-G4-IR	B6Hα-1-B5-IR	B6Hα-1-A2-IR	B6Hu-3-E9-IR	B6Ha-3-F11-IR	B6Hα-4-H8-IR	B6Ha-2-C9-IR	B6Hu-2-C4-IR	B6Hu-2-C5-IR	B6Hα-1-A6-IR	Clone Design
GCAAVVAEASGDDPFYHKLSELLQGC	GCAEIVIEEGDDSDPFYHKLSELLQGC	GQCAMEEI I RGANDPFYHKLSELCEGG	GCTEVVGSGDDPFYHKLSELLQGC	GCAMVEATEGRRHDPFYHKLSELIQGC	CGEVTGRAGDPFYHKLSELLQGC	GCAAVETTTNGRNDPFYHKLSELLQGCR	GCAEVKAVKGAGDDPFYHKLSELL <u>Q</u> GC	GCAEIEIAAGGGGDPFYHKLSELLQGC	GCEEVEAETTGHRDPFYHKLSELLQGC	CGGAVPDGDDPFYHKLSELMQGC	RSMMAKAIVGGPGDPFYHKLYELQFGSR	GCKKVEAKKGNDADPFYHKLSELLQGC	CCTTEMVVMDARDDPFYHKLSELVTGG	RGCNDDGGKGWSDDPFYHKLSELICGG	RCEEKQAEVGPSSDPFYHKMSELLGCR	RGMKEEVLVGGSTDPFYHKLSELLQGS	WWQKKSGDGASASDPFYHKLSELIWGS	RCMVETIAVGSGDDPFYHKLSELCQGG	RCGRW*AEMGAGDDPFYHKLSELVCG	RGEVATMEVPAGGDPFYHKLSELLWGS	GCKMEETETGTSDDPFYHKLSELCSGG	Sequence oouuuuuuuuuuuuuuubeyhkLseLxxoo

Ratios ov	_ <b>=</b>	und	Compa	arisons
Ç-1 a8	ICTSK	: 5		
49.7	34.5	4.0	8.6	0.1
42.6	34.2	3.3	10.4	0.1
20.7	9.9	0.9	11.0	0.1
47.4	32.6	2.8	11.6	0.1
36.3	28.1	2.4	11.7	0.1
49.5	18.7	1.6	11.7	Q.1
44.6	24.2	1.7	14.2	0.1
22.3	14.6	1.0	14.6	0.1
41.5	20.5	1.0	20.5	0.0
36.4	28.4	36.0	0.8	1.3
36.7	27.9	34.7	0.8	1.2
34.9	32.1	35.6	0.9	1.1
36.3	33.7	37.3	0.9	1.1
34.7	33.7	• .	0.9	1.1
35.9	35.1	37.4	0.9	1.1
37.6	36.2	39.0	0.9	1.1
39.2	37.2	41.0	0.9	1.1
41.3	38.0	43.0	0.9	1.1
39.0	38.3	40.7	0.9	1.1
38.8	38.4	41.3	0.9	1.1
36.7	39.2	41.5	0.9	1.1
41.5	40.0	42.2	0.9	1.1
Ó	40.3	42.7		1.1

FIGURE 2H (Con't)



B6Hβ-3-C4-IR B6Hβ-3-G7-IR B6Hβ-3-C11-IR	В6Hβ-3-C3-IR В6Hβ-3-B5-IR	B6Hβ-3-C12-IR B6Hβ-3-B11-IR	B6Hβ-3-A2-IR B6Hβ-3-A8-IR	B6Hβ-3-C5-IR	B6Hβ-3-E12-IR	B6Hβ-3-A4-IR	B6Hβ-3-B4-IR	₿6Hβ-3-A12-IR	B6H()-3-B7-IR	B6H()-3-D8-IR	B6H()-3-A11-IR	В6Hβ-3-C8-IR	B6Hβ-3-C2-IR	В6H(}-3-H11-IR	В6Hβ-3-A5-IR	В6Нβ-3-Н1-IR	в6нβ-3-G5-IR	В6H(}-3-B2-IR	B6Hβ-3-D7-IR	Design	Clone
GCIIAEKVVGPPDDPFYHKLSELLDCG GCEKVVAVAGNAGDPFYHKLSELLQGC GSVMTVTEMAGADDPFYHKLSELLQGGR	GGAAVVVAMGGNDDPFYHKLFELMQGG GGVIKAMKAGGPDDPFYHKLSELLQGS	LCDEKQRVTGGTNDPFYHKLSELTGGCR SCMVEGPNDDPFYHKLSELLQGCR	RSVTAKVEVGSDRDPFYHKLSELLQGS GSRRQKIEVGTPNDPFYHKLSELLQGG	CSTVTVSGSDDPFYHKLSELLQGC	GCKVDDE*ARSSDPFYHKLSELLKGCR	GCAVTTMTMRSPADPFYHKLSELCQGR	GSVAAAKKTGSSDDPFYHKLFELLQGS	WLCDRDGRDEQPWDPFYHKLSELVSCGR	RSĄĄKĄVIGSPNDPFYHKLSELIQGG	WQRNKQQIIGTPDDPFYHKLSELLEGS	CSVAVGDSGDPFYHKLSELLQGCR	SCAAEKEVAGTARDPFYHKLSELMQSS	GCAAVVKETHDPPDPFYHKLSELLHGC	GCAAIAVATGNDNDPFYHKLSELLQGCR	SSKVVKATVGTPHDPFYHKLSELL <u>Q</u> GS	WLCKRQTHDPDPFYHKLSELAGCR	RGGDGDPFYHKLFELMQSS	CSAVKMAEAGDPSDPFYHKLSELCQGS	RGVEMKAIVVGTPNDPFYHKLSELSSGS	OOUUUUUUJJJJDPFYHKLSELXXOO	Sequence

																							•				
29.2	4.1	41.1	42.7	43.0	40.7	39.8	40.0	41.1	40.7	40.8	35.8	40.1	39.0	33.5	37.8	35.4	40.4	37.0	37.4	37.7	34.9	36.8	35.3	34.3	39.5	1	Ratios over E-Tag
30.6	2.4	42.3	43.9	42.7	42.6	42.0	41.9	41.4	40.9	40.7	40.7	40.4	39.8	39.4	39.0	38.3	38.2	37.7	36.5	36.4	35.5	35.4	35.0	34.4	27.1	1	Ratios over Background E-Tag IGFsR II
28.2	2.1	36.6	45.4	44.0	43.3	41.3	41.6	41.9	42.6	39.5	40.7	41.1	41.1	41.3	39.4	39.5	39.1	39.5	37.2	37.6	35.9	36.5	35.6	35.4	26.3		~
1.1	1.1	1.2	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	;	Comparisons IGFR/IR IR/IC
0.9	0.9	0.9	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1	sons IR/IGFR

FIGURE 2II (Con't)



В6H(}-3-C7-IR	В6Нβ-3-D6-IR	₿6Hβ-3-B9-IR	B6Hβ-3-B10-IR	₿6Нβ-3-A7-IR	B6H }-3-G6-IR	в6нβ-3-Ф1-IR	В6Hβ-3-D2-IR	в6нβ-3-В12-IR	в6нβ-3-D5-IR	В6Hβ-3-F10-IR	β6Hβ-3-G10-IR	в6нβ-3-н12-ІR	Clone Design
RCKGIKAHSDNDPFYHKLSELCQGG	GSKVKAMAVGTSDDPFYHKLSELVQGR	GCAVTAITINGTSDPFYHKLSELCOGS	GGEARRROOVGTANDPFYHKLSELAFGGR	CSVVMTEEKNDRDDPFYHKLSELLQGC	RCEEITIGDGRAGDPFYHKLSELLQGC	WCDQKETVVSNSDDPFYHKLSELVGCS	RRITIKVKAGDDDDPFYHKLSELLWGG	GCKEVVVETAHADDPFYHKLSELLQGCR	SRTGERQVVGSHADPFYHKLSELLLSS	GCAAVVVTTGGDNDPFYHKLSELLQGCR	GCEEVVVMANSSADPFYHKLSELCQGSR	RGEAKEAKIGSAGDPFYHKLSELMQGSR	Sequence OOUUUUUUUJJJJDPFYHKLSELXXOO

·	Ratios over E-Tag	er Background IGFsR II	ųnd IR	Compai IGFR/IR	risons IR/IGFR	
		1	1	1	:	
	33.6	32.0	29.5	1.1	0.9	
	30.1	34.3	30.5	1.1	0.9	
	37.1	35.3	32.4	1.1	0.9	
	39.9	38.9	35.5	1.1	0.9	
	39.5	40.0	37.1	1.1	0.9	
	40.4	41.5	39.1	1.1	0.9	
	41.1	44.6	36.6	1.2	0.8	
	34.3	36.4	24.1	1.5	0.7	
	38.1	30.9	18.4	1.7	0.6	
	32.3	36.5	22.8	1.6	0.6	
	38.6	38.5	20.8	1.9	0.5	
	35.9	36.0	15.6	2.3	0.4	
	38.3	38.0	6.6	5.8	0.2	



!						
		:	16.4	14 2	GSVITKAMKADGDDPFYHKLSELL*GG	B6H-3-H3-IGFR
1	!	:	16.6	10.1	RKTAMVVIGDASDPFYHKLSELAFGS	B6H-4-H3-IGFR
:	:	:	16.8	9.0	RGAQSPDPFYHKLSELAFGS	B6H-3-B3-IGFR
\$ 1	;	!	17.1	14.6	CCIAMVEMAAGGGDPFYHKLSELLSGR	B6H-3-C3-IGFR
1		!	17.2	16.8	GRKMEIVAIRGAHDPFYHKLSELL*GR	B6H-3-C4-IGFR
1	;	:	18.5	16.2	RRMVMEAAENHADDPFYHKLSELLWRD	B6H-3-C2-IGFR
1	:	:	18.9	23.6	RREVAIVAAGAGGDPFYHKLSELLSRG	B6H-4-C3-IGFR
ł	:	:	19.2	12.5	SSAIIMVAADRADDPFYHKLSELLWGS	B6H-4-E6-IGFR
1	:	:	19.2	14.1	RREKKVKVTTTDNDPFYHKLSELVFGG	B6H-4-A9-IGFR
:		:	19.3	12.1	GGKTAVEVTSPASDPFYHKLSELLLRG	B6H-3-D2-IGFR
1		;	20.3	12.5	RRKMATEIMRSDADPFYHKLSELLGGS	B6H-4-F3-IGFR
:		:	20.6	20.0	RGVATVVVANHHSDPFYHKLSELVLRG	B6H-3-E1-IGFR
•	:	:	20.8	14.2	GRVVVAAAVRPDDDPFYHKLSELVAGR	B6H-3-E3-IGFR
1	:	:	20.9	11.3	RRTTVMETVGGRDDPFYHKLSELLHRG	B6H-4-F9-IGFR
;	:	;	21.4	19.1	RGVVIETTKDPGADPFYHKLSELLFGR	B6H-4-G3-IGFR
;	;	;	21.7	15.9	RSVIAN???G?NADPFYHKLSELISSG	B6H-3-B1-IGFR
1	:	:	21.8	11.6	RRVTAVIEVDGADDPFYHKL?ELLSGG	B6H-3-E2-IGFR
:	:	!	21.9	14.5	SR.MAMVEVGNPGDPFYHKLSELLGS	B6H-3-B2-IGFR
•	;	;	22.5	15.2	GGVVAVVAAGRRDDPFYHKLSELVSGR	B6H-3-G2-IGFR
1	;	:	22.5	14.0	RGTAKQRKSSDP*DPFYHKLSELIYGS	B6H-4-D11-IGFR
:	:	:	22.8	10.2	SRKEVTEMVGGPSDPFYHKLSELMGSG	B6H-3-B4-IGFR
1	:	:	22.8	13.0	RRMAGWQ*TSSSDPFYHKLSELVSGS	B6H-3-A4-IGFR
!	1	:	22.8	14.2	GRTEEVVVVGTRRDPFYHKLSELLASG	B6H-3-A3-IGFR
:	:	1	24.2	20.0	RSTTMVKAVPPPRDPFYHKLSELL*GG	B6H-3-D1-IGFR
i i	•	:	24.8	12.5	SREAVEVTMARGSDPFYHKLSELVWGS	B6H-3-F2-IGFR
i,	;	:	25.2	14.2	GGAVIVTAARRGSDPFYHKLSELVGRG	B6H-3-G3-IGFR
1	;	:	27.6	19.0	RSTMKEKIEGDGNDPFYHKLSELLKSG	B6H-3-D4-IGFR
;	;	!	30.8	20. Q	RRVAAVA?KDATGDPFYHKLSELLRSG	B6H-3-F1-IGFR
	;	:	1 1 1	!	OOUUUUUUJJJJJDFYHKLSELXXOO	Design
IGFR/IR IR/IGFR	IÇFIVI	IR	IGFsR	E-Tag	Sequence	Clone
Comparisons	Com	pnyo	ver Background	Ratios ov		



B6H-4-A3-IGFR F B6H-4-H10-IGFR F B6H-3-G1-IGFR C	-E1-IGFR -C1-IGFR		B6H-4-B7-IGFR S B6H-4-A7-IGFR C	B6H-4-H9-IGFR F			B6H-3-A2-IGFR C	- IGFR	B6H-4-B2-IGFR C	B6H-4-F5-IGFR F	B6H-4-E10-IGFR C	B6H-4-D6-IGFR C	₿6H-4-D8-IGFR (	Clone Spesign C
GRKKAVATMTDGGDPFYHKLSELILRS RGETEMAVADTDDDPFYHKLSELLGRG GQRDPFYHKLSELMGRGA	GCAEVEEVAGAGHDPFYHKLSELV?SG SSVVVVEVVDARRDPFYHKLSELV?SG	RGA I GNAAVGNRSDPFYHKLSEL I SRG GGM I KTAMEHDTRDPFYHKLSELLRGG	SGTVTVIAMSGTDDPFYHKLSELLSRS GRTAVVKEASPAHDPFYHKLSELLLRG	RGVEVAVITHGPPDPFYHKLSELLRGA	RRW*KVPGAADPFYHKLSELLGRSA	SCVMVETVAGRNRDPFYHKLSELVGGC	GGMAEVVVVGPPRDPFYHKLSELVGGG GGEVKVMVADGSTDPFYHKLSELLGRT	SGEGEMAMPGPDDPFYHKLSELIGSRA	GGMATKIVTAPGHDPFYHKLSELLFGG	RGKTKMAMAAGGNRDPFYHKLSELIFGN	GGAKVAVVVDHGDDPFYHKLSELLRGS	CCEMVKTIEHGGNDPFYHKLSELVFGR	GGVKAAAAERDDSDPFYHKLSELLFGS	<b>ეისისის განისის განისის განისისის განისისის განისისისის განისისისის განისისისის განისისისის განისისისის განისისისის განისისისის განისისისის განისისისის განისისისისის განისისისისისისისისისისისისისისისისისისის</b>

2.4	4.4	4.4	5.7	3.6	5.2	4.4	9.7	6.4	12.3	6:7	7.2	4.4	5.9	10.9	8.2	6.6	12.3	10.2	12.6	15.1 16.4	:	E-Tag	Ratios ov
2.9	3.2	4.2	4.6	7.1	7.4	7.8	8.1	8.2	8.4	8.6	8.7	9.5	9.6	9.9	11.6	11.8	14.8	15.1	15.6	16.4	:	IGFsR	er Backgro
;		:	!	;	!		;	:	;	;	;	:	:	1	;	;	•	;	:	!	!	₹	pund
:	† 	!	1		1	1	1	!	1	1	:	1	1	!	i	:	:	4 1	;	;	:	IGFR/IR	Compa
	1	1	1	1	1	r I	1	;	1	1	:	;	;	1	i	,	;	1	1			IIVIGER	risons

FIGURE 21 (Con't)



EHWNTVDPFYQGLWELLRESG	B6C-4-E8-IR
EHWNTVDPFYQRMFELLRE	B6C-4-E9-IR
<u>EHWNTVDPFYQLLFELLRE</u>	B6C-3-A12-IR
EHWNTVDPFYY*MSELLRE	B6C-3-B12-IR
EHWNTVDPFYH*MSNLLRE	B6C-4-H2-IR
EH*NTVDPFYHKLYELLRE	B6C-4-F7-IR
EHWNTVDPFYLMLQQLLRE	B6C-3-D5-IR
EHWNTVDPFYQQLFELLRE	B6C-3-C2-IR
<b>EHWNTVDPFYGKLQELLRE</b>	B6C-3-C12-IR
EHWNTVDPFYDGLRQLLRE	B6C-3-B8-IR
<b>EHWNTVDPFYNLLQELLRE</b>	B6C-3-B11-IR
EHWNTVDPFYD*MRNLLRE	B6C-4-F6-IR
EHWNTVDPFYQALFELLRES	B6C-3-B1-IR
EHWNTVDPFYYGLQTLLRE	B6C-3-B3-IR
EHWNTVDPFYQYFSELLRE	B6C-3-C10-IR
EH*NTVDPFYQGLFELLRE	B6C-3-D6-IR
EH*NTVDPFYEGLLELLRE	B6C-3-C8-IR
EHWNTVDPFYQFFAELLRE	B6C-4-G7-IR
EHWNTVDPFYH*ISELLRE	B6C-3-D8-IR
<b>EHWNTVDLFYYGLQELLRES</b>	B6C-3-C6-IR
EHWNTVDPFYRQLYEWLRE	B6C-4-G4-IR
EHWNTVDPFYHOMYEWLRES	B6C-3-D9-IR
EHWNTVDPFYHYFQELLRE	B6C-3-A11-IR
EHWNTVDPFYRQLSEWLRES	B6C-4-H4-IR
EHWNTVDPFYQQLYEWLRE	B6C-4-H11-IR
EHWNTVDPFYHQLSEWLRE	B6C-3-A2-IR
EHWNTVDPFYNQLWEWLRE	B6C-4-F2-IR
EHWNTVDPFYFTLFE*LRE	B6C-3-C7-IR
EHWNTVDPFYHKLSELLRE	<b>Девідп</b>
Sequence	Clone

	Ratios ov	Ratios over Background	e e	Comparisons	isons
	: ;	1 4	;	: .	: ;
	31.7	2.1	20.0	0.1	9.4
	8	1.8	4.3	0.4	2.4
	34.9	18.1	36.0	0.5	2.0
		28.2	38.6	•	1.4
	39.5	28.3		0.7	1.4
	S	5	34.2	0.8	1.3
	35.7	30.3	37.2	0.8	1.2
	IJ	31.0	38.4	0.8	1.2
	w	w	•	0.9	1.1
	4	Φ	•	0.9	1.1
•	ū	Œ	8.		1.1
	S	-1	•	0.9	1.1
	7	7	0.		1.1
	U)	9	0	0.9	1.1
	æ	8	0.	0.9	1.1
	J	æ	1.	0.9	1.1
	LΠ	9	8.	1.0	1.1
	σ	7	8	1.0	1.1
	-1	39.2		1.0	1.1
	œ	80	8.	1.0	1.0
	4	4	w.	1.0	1.0
	w	ហ	4.	1.0	1.0
	4	4	4.	1.0	1.0
	L)	S	5	1.0	1.0
	w	ū	9.	1.0	1.0
	33.1	37.0	6	1.0	1.0
	σ	σ	6.	1.0	1.0
	4	Ū.	<u>ه</u>		1.0



EHWNIVUPFYHMLQXLLXESG	86C-3-C3-1K
ALLRE	6C-3-A5-I
EHWNTVDPFYH*MSELLRESG	÷
EHWNTVDPFYHGLQELLRESG	B6C-3-A10-IR
EHWNTVDPFYQKLQDLLRESG	B6C-3-B10-IR
EHWNTVDPFYQGLLDLLRESG	B6C-4-H8-IR
EHWNTVDPFYN*MRELLRESG	B6C-4-G9-IR
EHWNTVDPFYQGL1ELLRESG	B6C-4-F12-IR
EHWNTVDAFYHGLQELLRESG	B6C-3-A7-IR
EH*NTVDPFYHGLYELLRESG	B6C-3-A9-IR
EHWNTVDPFYD*IADLLRESG	B6C-4-G8-IR
EHWNTVDPFYLGLQELLRESG	B6C-4-F10-IR
EHWNTVDPFYHGL*ELLRESG	B6C-3-D11-IR
EHWNTVDPFYH*MRELLRESG	B6C-4-H7-IR
EHWNTVDPFYAKLQELLRESG	B6C-3-B9-IR
EHWNTVDPFY <u>Q</u> GLFELLRESG	B6C-3-D12-IR
EHWNTVDPFYHYMSQLLRESG	B6C-3-D10-IR
EHWNTVDPFYH*MTELLRESG	B6C-4-H1-IR
EHWNTIDPFYHQISELLRESG	B6C-3-A8-IR
EHWNTVDPFYQKLQELLRESG	B6C-4-G5-IR
EHWNTVDPFYLKMQDLLRESG	₿6C-3-C1-IR
EHWNTVDPFYLMLQELLRESG	B6C-3-D4-IR
EHWNTVDPFYQALQQLLRESG	B6C-3-D1-IR
EHWNTVDPFYQGLSELLRESG	B6C-3-A6-IR
EHWNTVDSFYLGLQELLRESG	₿6C-4-F9-IR
EHWNTVDPFYHYLQDLLRESG	B6C-4-H12-IR
EHWNTVDPFYH*MSDLLRESG	₿6C-4-Ę5-IR
EHWNTVDPFYHMLQELLRESG	B6C-3-B6-IR
EHWNTVDPFYHLLQELLRESG	B6C-3-C4-IR
EHWNTVDPFYD* I SELLRESG	₿6C-3-C11-IR
EHWNTVDPFYHKLSELLRESG	Design
Sequence	Clone

																															<u>.</u>	₹:
34.5	m	NO.	œ	S	œ	J	œ	œ	σ	LD.	7	6	J	6	6	37.0	9	4	9	9	S	9	35.8	36.1	37.0	35.5	•	34.5	33.4	;	ag. Tag	Ratios ove
	•	•	0.	0.	40.0	9.	38.4	9	8	8	8	7.	8	7.	7.	7.	6.	7.	7.	9	9	7.	38.0	6.	9	5	9	5	35.0	1	IGFsR	r Backgrou
			•	40.9	40.8	40.5	40.2	40.2	39.9	39.7	39.3	39.2	39.1	38.8	38.7	38.5	38.3	38.1	38.0	37.9	37.5	37.5	37.4	37.3	37.1	36.9	36.9	36.8	•	:	₹	ņģ
1.1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1	IGFR/IR	Compar
0.9	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	.1.0	;	HVIGER	SONS

FIGURE 2J (Con't)



B6C-3-A4-IR	B6C-3-B5-IR	B6C-3-A1-IR	B6C-3-D2-IR	B6C-4-F4-IR	Design	Clone
EHWNTVDPFYRRLQELLRESG	EHWNTVDPFYHKLQELLRESG	EHWNTVDPFYH*LNELLRESG	EHWNTVDPFYH*LAELLRESG	EHWNTVDPFYQKLFELLRESG	EHWNTVDPFYHKLSELLRESG	Sequence

33.6	33.4	26.5	8.5	36.3	;	Ratios ov E-Tag
31.8	33.0	30.7	10.3	36.9	1	Ratios over Background E-Tag IGFsR II
13.5	15.0	16.8	9.0	34.3	:	<b>≂</b>
2.4	2.2	1.8	1.2	1.1	;	Compai IGFIVIR
0.4	0.5	0.5	0.9	0.9	:	arisons R IR/IGFR



Peptide 5.1 (18 aa)	Clone B6 P
NTVDPFYHKLSELLREKK (biotin	AETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA

reptide 5.2 (17 dd)	Clone FA
QMRDIE ISELASEARK (DIOCIN)	MILICVER FOLLEW DEPKIN CVOMKD FRYSTIAST

Peptide 5.3 (14 aa)	Clone D5
ADK <b>NFYDWF</b> MAAKK (biotin)	PLYGGGIHLYYPGTMGYVPGFPRQVKVLGDADK <b>NFYDWF</b> M

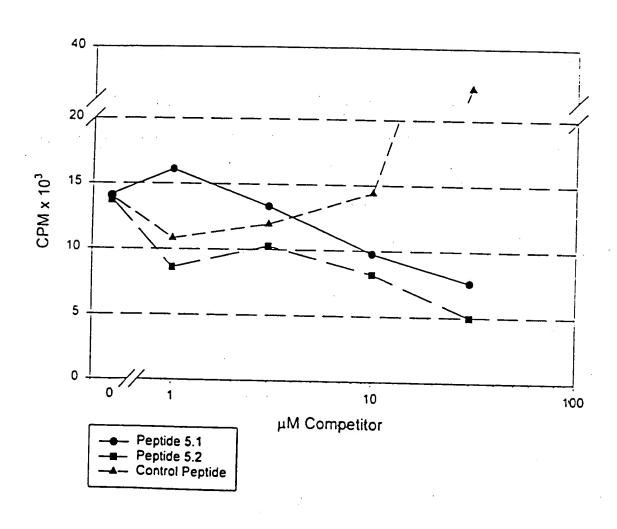
YRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDWFV SAKNEYDWEVKK (biotin)

Clone A6

Peptide 5.4 (12 aa)

FIGURE 21







EHWNTVGAFQPTPEYLLRESGA	B6C-3-G1-IGFR
EHWNTVDPFLDKRS*LLRESGA	B6C-3-H12-IGFR
EHWNTVATF*DKVTDLLRESGA	B6C-3-E12-IGFR
EHWNTVDPFYHKLQELLRESGA	B6C-3-A1E-IGFR
EHWNTVRPRYQ*LSELLRESGA	B6C-3-H11-IGFR
EYWNTVDPFYHKLAELLRESGA	B6C-3-H10-IGFR
EHWNTVDPFYDKLSDLLRESGA	B6C-3-A7-IGFR
EHWNTVDPFYHKLAELLRESGA	B6C-3-F9-IGFR
EHWNTVDQFYQALFELLRESGA	B6C-3-D3-IGFR
ERWNTVDPFYHKLSELLRESGA	B6C-3-A4-IGFR
EHWNTVEPFGA*LAEPLRESGA	B6C-3-D5-IGFR
EHWNTVDPF * PKVSELLRESGA	B6C-3-B6-IGFR
EHWNTVDPFYDRLTELLRESGA	B6C-3-F2-IGFR
EHWNTVEP*YHKLCGRLRESGA	B6C-3-F8-IGFR
EHWNTVDPFYHILAELLRESGA	B6C-3-E11-IGFR
EHWNTVDPFYARLSALLRESGA	B6C-3-C12-IGFR
EHWNTVDPFYAKLSALLRESGA	B6C-3-F10-IGFR
EHWNTVDPFYQKLSELLRESSA	B6C-3-F7-IGFR
EHWNTVDPFYNKLSELLRESGA	B6C-3-C10-IGFR
EHWNTVDPFYHNLYELLRESGA	B6C-3-A9-IGFR
EHWNTVDPFYHRLSELLRESGA	B6C-3-A2-IGFR
EHWNTVDPFYHGLQELLRESGA	B6C-3-A8-IGFR
EHWNTVDPFYQRLFELLRESGA	B6C-3-C8-IGFR
EHW?TVDPFYLKLSELL?ESGA	B6C-3-C9-IGFR
EHWNTVDPFYQKLSELLRESGA	B6C-3-A3-IGFR
EHWNTVDPFYHKLYELLRESGA	₿6С-3-Ф4-IGFR
EHWNTVDPFYHKLEELLRESGA	B6C-3-F5-IGFR
EHWNTVDPFYLKMTELLRESGA	B6C-3-C4-IGFR
EHWNTVDPFYHKLSELLRESGA	<b>Design</b>
Sequence	Clone

2.3	2.7	23.3	2.3	17.1	14.4	24.8	28.0	22.6	2.4	2.9	30.8	25.4	28.0	28.4	27.4	27.3	30.0	33.0	33.6	29.7	30.5	29.6	29.7	26.6	26.5	21.0	:	Ę-Tag	Ratios ov
9.9	10.1	10.5	11.0	11.1	12.8	13.6	13.8	13.9	14.3	14.7	15.1	16.0	17.2	17.3	17.4	17.6	17.7	18.3	19.0	19.7	19.9	20.5	20.8	22.1	22.6	23.1	;	<b>IÇFSR</b>	Ratios over Background
1	;	:	!	!	I I	•	!	!	!	!	1	1	1	1	1	:	1	1	1	1	!	1	1	:	!	1	;	IR	φnφ
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1		•	1	1	1	•	1	1	1	1	1	1	1	1	•	:	1	!	1	:	1	:	t I		:	į	!	JIR IR/IGFR	isons

FIGURE 2K



Parental Design 20E2A-3-B6-IR 20E2A-4-E2-IR 20E2A-4-F9-IR 20E2A-3-C9-IR 20E2A-4-F7-IR 20E2A-3-A7-IR 20E2A-4-G5-IR 20E2A-3-A3-IR 20E2A-4-F4-IR 20E2A-4-E9-IR 20E2A-4-H11-IR 20E2A-4-G7-IR 20E2A-3-C11-IR 20E2A-4-F11-IR 20E2A-3-D8-IR 20E2A-4-H1-IR 20E2A-4-E4-IR 20E2A-3-A5-IR 20E2A-4-G10-IR 20E2A-3-B2-IR 20E2A-3-C1-IR 20E2A-4-E3-IR 20E2A-3-C4-IR 20E2A-4-H3-IR 20E2A-4-E7-IR MPMGLNFYDG1EQLVREWGGD GGTDQLFYGAIDQLVGGTWWR SPWGRAFYDALDQLMGGAERG TISAHTFYEAIYQLIEGIDPL RDAGSSFYDAIDQLVCLTYFC PPWGARFYDAIEQLVFDNLCC FYDAIDQLVRGSARAGGTRD XXXXXXFYDAIDQLVXXXXX GDARDPFYDAMEQLVYGELGG HGVPRTFYDAIDQLVWGIEVG LSPPRDFYDAIQQLVRDGGWG IGRVRSFYDAIDKLFQSDWER RKPCQTFYDCILDLVVTDVDV VASPRSFYEATAQLVFNLGQE LSVHQSFYDAINELIFSGLEA QGNAQNFYDAIDQLCFGCLGG HHSAFSFYDAIAQLVGVPWEE QCNPRTFYEAIAQLVTGCDVS <u>APIPFSFYDAIVQLVMQGDHE</u> AVFPRTFYEAIDQLVGVSLLG PAGCQGFYEAIEQLVTGGECG LLSRWTFYDAIEQLVGGGADG SSEGWTFYDAIDQLVGRERGW FTYVHSFYDAIEQLVRGEGGG VSTSGSFYDAIQQLLEDSWGW PDGCATFYHAI QQLVTGFPCV RGPPMTFYDAIAQLVAQSADG

17.8	18.5	25.2	י ה	24.5	24.6	21.5	24.6	23.4	23.2	22.3	24.4	22.1	21.0	21.0	12.6	4.7	25.4	17.2	14.8	24.4	20.1	•	14.5	13.9	19.9	30.6	1	E-Tag	Ratios over Baci
16.6	15.7	1.1.	ر د د	24.1	23.4	22.9	22.5	22.3	21.0	20.8	20.4	19.5	16.0	11.9	5.6	2.1	26.9	8. <sub>3</sub>	5.9	16.4	10.6	4.2	1.6	1.3	1.2	15.1	1	<b>IĢFsR</b>	Backgro
14.4	13.6							22.5							5.7	2.1	S	8.9	6	23.8	15.8	15.2	6.1	9.7	13.9	4.2	1	IR	pun
1.2								1.0										0.9	0.9	0.7	0.7	0.3	ο.ω	0.1	0.1	3.6		IGFR/IR	<u> </u>
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R GGDGDPFYDWIEQLVRAGS R LDLCASFYDAIEQLVRAGS R WLACQSFYDAIDQLINGGE R EVNALSFYDAIDQLVRGGL R RLQPRTFYEAIDQLVRGGL R SGAHRTFYDAIQELVGMGG R NMQSLTFYDAIQLVLGRS IR RAVGATFYDAIQLVTGVN DRLAFSFYDAIDQLVTGVN R GGSVLSFYDAIDQLVGGSW IR GGSVLSFYDAIDQLVGGSW IR GGSVLSFYDAIEQLVLGRL R CAQPESFYDAIDQLVSGQA R AQFPRTFYDAIDRLVTGRC R QRRARDFYEAIQQLVGGVA IR QRRARDFYEAIQCLVGGVA IR PLVRGTFYDAIEQLVRGSP R QRRARDFYDAIEQLVRGSP R QRRARDFYDAIEQLVGGSAL IR PRGQASFYDAIEQLVGGFE R PRGQASFYDAIEQLVGGFE R PRGQASFYDAIEQLVGGFE R PRGASFYDAIEQLVGGFE R PRGASFYDAIEQLVGGFE R PRGASFYDAIEQLVGGFE R PRGASFYDAIEQLVGGFE R PRGASFYDAIEQLVGGGG R PAIGFTFYDAIRELVGGGG	
R GGDGDPFYDWIEQLVRA R LDLCASFYDAIEQLVRA R WLACQSFYDAIDQLING R EVNALSFYDAIDQLVRG R EVNALSFYDAIDQLVRG R RLQPRTFYDAIQELVGM R NMQSLTFYDAIAQLVLG R RAVGATFYDAIDQLVRK SQCRGGFYDAIYQLVTG R SQCRGGFYDAIDQLVRG R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIDQLVGG R CAQPESFYDAIDQLVGG R AQFPRTFYDAIDQLVGG R ORRARDFYEAIQOLVGG R ORRARDFYEAIQOLVGG R ORRARDFYDAIQQLVGG	0E2A-4-E11- 0E2A-3-A4-I 0E2A-3-A4-I 0E2A-3-B7-I 0E2A-3-B7-I 0E2A-4-G11- 0E2A-4-E8-I 0E2A-4-H2-I 0E2A-4-H2-I 0E2A-3-D4-I 0E2A-3-B9-I 0E2A-3-D10-I 0E2A-3-D6-I 0E2A-3-D6-I 0E2A-4-G9-I
R GGDGDPFYDWIEQLVRAGR R LDLCASFYDAIEQLVRAGR R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLURGG R RLQPRTFYDAIDQLURGG R RLQPRTFYDAIQLUVLGR R SGAHRTFYDAIAQLVLGR R NMQSLTFYDAIAQLVLGR R RAVGATFYDAIDQLVRKD R GGSVLSFYDAIDQLVRGG R GGSVLSFYDAIDQLVLGGR R GGSVLSFYDAIEQLVLGR R CAQPESFYDAIDQLVSGQ R CAQPESFYDAIDRLVTGR R ORRARDFYEAIQQLVGGV R ORRARDFYDAIRQLVGGV R ORRARDFYDAIRQLVGGS R ORRARDFYDAIRQLVGGS R ORRARDFYDAIRQLVGGSA R PLVRGTFYDAIEQLVGGSA DGRVWSFYDAIEQLVGGSA DGRVWSFYDAIEQLVGGSA DGRVWSFYDAIEQLVGGSA DGRVWSFYDAIEQLVGGSA DGRVWSFYDAIEQLVGGA	0E2A-4-E11- 0E2A-3-A4-I 0E2A-3-A4-I 0E2A-3-B7-I 0E2A-3-B7-I 0E2A-4-G11- 0E2A-4-E8-I 0E2A-4-H2-I 0E2A-4-H2-I 0E2A-3-D4-I 0E2A-3-B9-I 0E2A-3-D10-I 0E2A-3-D10-I 0E2A-3-D6-I
R GGDGDPFYDWIEQLVRA R LDLCASFYDAIEQLVGV R WLACQSFYDAIDQLING R EVNALSFYDAIDQLVRG R RLQPRTFYEAIDQLVRG R NMQSLTFYDAIQELVGM R NMQSLTFYDAIQLVLG R RAVGATFYDAIDQLVLG R GGSVLSFYDAIDQLVHC R GGSVLSFYDAIDQLVHC R GGSVLSFYDAIDQLVHG R GGSVLSFYDAIDQLVGG R ORRARDFYEAIQQLVGG R ORRARDFYDAIQQLVGG R ORGOASFYDMIEQLVGG R OGRVWSFYDALEQLVGG	0E2A-4-E11- 0E2A-3-A4-I 0E2A-3-A4-I 0E2A-3-B7-I 0E2A-3-B7-I 0E2A-4-G11- 0E2A-4-E8-I 0E2A-4-H2-I 0E2A-4-H2-I 0E2A-4-H4-I 0E2A-3-D4-I 0E2A-3-B10-I 0E2A-3-B10-I 0E2A-3-B10-I 0E2A-3-D10-I 0E2A-3-D10-I 0E2A-3-D10-I
R GGDGDPFYDWIEQLVRA R LDLCASFYDAIEQLVRA R WLACQSFYDAIDQLING R EVNALSFYDAIDQLVRG R RLQPRTFYEAIDQLVRG R NMQSLTFYDAIQELVGM R NMQSLTFYDAIQELVGM R NMQSLTFYDAIDQLVLG R RAVGATFYDAIDQLVLG R GGSVLSFYDAIDQLVHC R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIDQLVGG R CAQPESFYDAIDRLVTG R QRRARDFYEAIQQLVGG R ORRARDFYEAIQQLVGG R ORRARDFYDAIRQLVMG R VGIAWTFYDAIQQLVRG PLVRGTFYDAIQQLVRG VGIAWTFYDAIQQLVRG VGIAWTFYDAIQQLVRG	0E2A-4-E11- 0E2A-3-A4-I 0E2A-4-G8-I 0E2A-3-B7-I 0E2A-4-G11- 0E2A-4-E8-I 0E2A-4-H2-I 0E2A-4-H2-I 0E2A-4-H4-I 0E2A-3-D10- 0E2A-3-B9-I 0E2A-3-B10- 0E2A-3-B10-
R GGDGDPFYDWIEQLVRA R LDLCASFYDAIEQLVGV R WLACQSFYDAIDQLING R EVNALSFYDAIDQLVRG R RLQPRTFYEAIDQLVGG R NMQSLTFYDAIQELVGM R NMQSLTFYDAIAQLVLG R RAVGATFYDAIDQLVLG R GGSVLSFYDAIDQLVHC R GGSVLSFYDAIDQLVGG IR GGSVLSFYDAIDQLVLG R SGPMSFYDAIEQLVLG R CAQPESFYDAIDRLVTG R OAQFPRTFYDAIDRLVTG R OAQFPRTFYDAIDRLVTG R OAQFPRTFYDAIDRLVTG R OAQFPRTFYDAIDRLVTG R OARARDFYEAIQQLVGG R OARARDFYEAIQQLVGG PLVRGTFYDAIQQLVGG R OARARDFYEAIQQLVGG R OARARDFYEAIQQLVGG R OARARDFYEAIQQLVGG	0E2A-4-E11- 0E2A-3-A4-I 0E2A-3-A4-I 0E2A-3-B7-I 0E2A-3-G11- 0E2A-3-C5-I 0E2A-4-E8-I 0E2A-4-H2-I 0E2A-4-H4-I 0E2A-3-D4-I 0E2A-3-B10-I 0E2A-3-B10-I
R GGDGDPFYDWIEQLVRA R LDLCASFYDAIEQLVGV R WLACQSFYDAIDQLING R EVNALSFYDAIDQLVRG R RLQPRTFYEAIDQLVGG R NMQSLTFYDAIQELVGM R NMQSLTFYDAIAQLVLG R RAVGATFYDAIDQLVRK R SQCRGGFYDAIYQLVTG R GGSVLSFYDAIDQLVGG IR GGSVLSFYDAIDQLVGG R GGSVLSFYDAIEQLVLG R GGSVLSFYDAIDQLVGG R QGPPRTFYDAIDQLVGG R QGPPRTFYDAIDRLVTG R QAQFPRTFYDAIDRLVTG R QARARDFYEAIQQLVGG R PDECQSFYCAIDRLVTG	0E2A-4-E11- 0E2A-3-A4-I 0E2A-4-G8-I 0E2A-3-B7-I 0E2A-3-G11- 0E2A-3-C5-I 0E2A-4-E8-I 0E2A-4-H2-I 0E2A-4-H4-I 0E2A-3-D4-I 0E2A-4-F5-I 0E2A-3-B10-
R GGDGDPFYDWIEQLVRA R LDLCASFYDAIEQLVGV R WLACQSFYDAIDQLING R EVNALSFYDAIDQLVRG R RLQPRTFYEAIDQLVRG R NMQSLTFYDAIQELVGM R NMQSLTFYDAIQLVLG R SQCRGGFYDAIYQLVTG R SQCRGGFYDAIDQLVRK R SQCRGGFYDAIDQLVRG R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIDQLVGG R CAQPESFYDAIDQLVGG R CAQPESFYDAIDRLVTG R ORRARDFYEAIQQLVGG	0E2A-4-E11- 0E2A-3-A4-I 0E2A-4-G8-I 0E2A-3-B7-I 0E2A-4-G11- 0E2A-4-E8-I 0E2A-4-H2-I 0E2A-4-H2-I 0E2A-4-H4-I 0E2A-3-D4-I
R GGDGDPFYDWIEQLVRA R LDLCASFYDAIEQLVGV R WLACQSFYDAIDQLING R EVNALSFYDAIDQLVRG R RLQPRTFYEAIDQLVRG R NMQSLTFYDAIQELVGM R NMQSLTFYDAIQLVLG R RAVGATFYDQINQLVRK GCRGGFYDAIYQLVTG R GGSVLSFYDAIDQLVHC R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIEQLVLG R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIDQLVGG R CAQPESFYDAIDRLVTG R ODECQSFYCAIDRLVTG	0E2A-4-E11- 0E2A-3-A4-I 0E2A-4-G8-I 0E2A-3-B7-I 0E2A-4-G11- 0E2A-4-E8-I 0E2A-4-H2-I 0E2A-4-H4-I 0E2A-4-H4-I
R GGDGDPFYDWIEQLVRA R LDLCASFYDAIEQLVGV R WLACQSFYDAIDQLING R EVNALSFYDAIDQLVRG R RLQPRTFYDAIQELVGM R NMQSLTFYDAIQLVLG R RAVGATFYDQINQLVRK SQCRGGFYDAIYQLVTG R SQCRGGFYDAIDQLVHC R SQCRGFYDAIDQLVHC R SQCRGFYDAIDQLVHC R SGSVLSFYDAIDQLVGG R GGSVLSFYDAIDQLVGG R GGSVLSFYDAIEQLVLG R VSGCRTFYDAIDQLVSG R AQFPRTFYDAIDQLVSG R CAQPESFYDAIDRLVTG	0E2A-4-E11- 0E2A-3-A4-I 0E2A-4-G8-I 0E2A-3-B7-I 0E2A-4-G11- 0E2A-4-E8-I 0E2A-4-E8-I 0E2A-4-H2-I 0E2A-4-H4-I
R GGDGDPFYDWIEQLVRA R LDLCASFYDAIEQLVGV R WLACQSFYDAIDQLING R EVNALSFYDAIDQLVRG R RLQPRTFYDAIQELVGM R NMQSLTFYDAIAQLVLG R RAVGATFYDAIAQLVLG R RAVGATFYDAIDQLVRK SQCRGGFYDAIYQLVTG R GGSVLSFYDAIDQLVHC R GGSVLSFYDAIDQLVLG R GGSVLSFYDAIEQLVLG R VSGCRTFYDAIDQLVLG R VSGCRTFYDAIDQLVSG R OVSGCRTFYDAIDQLVSG R OVSGCRTFYDAIDQLVSG	0E2A-4-E11- 0E2A-3-A4-I 0E2A-4-G8-I 0E2A-3-B7-I 0E2A-3-C5-I 0E2A-4-E8-I 0E2A-4-E8-I
R GGDGDPFYDWIEQLVRAG R LDLCASFYDAIEQLVRGG R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLVRGG R RLQPRTFYEAIDQLIGGV R SGAHRTFYDAIQELVGMG R NMQSLTFYDAIAQLVLGR R NAVGATFYDAIYQLVTGV R SQCRGGFYDAIDQLVHCC R GGSVLSFYDAIDQLVGGS R GGSVLSFYDAIEQLVLGGG R RSGPMSFYDAIEQLVLGG	0E2A-4-E11- 0E2A-3-A4-I 0E2A-4-G8-I 0E2A-3-B7-I 0E2A-4-G11- 0E2A-3-C5-I 0E2A-4-E8-I
R GGDGDPFYDWIEQLVRAG R LDLCASFYDAIDQLINGG R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLVRGG R RLQPRTFYEAIDQLIGGV R SGAHRTFYDAIQLVLGRG R NMQSLTFYDAIAQLVLGR R NAVGATFYDQINQLVRKD R SQCRGGFYDAIDQLVHCC R GNRQRGFYDAIDQLVHCG R GGSVLSFYDAIAQLVGGG R GGSVLSFYDAIEQLVLGR	0E2A-4-E11- 0E2A-3-A4-I 0E2A-4-G8-I 0E2A-3-B7-I 0E2A-4-G11- 0E2A-3-C5-I
R GGDGDPFYDWIEQLVRAG R LDLCASFYDAIEQLVGVK R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLVRGG R RLQPRTFYEAIDQLIGGV R SGAHRTFYDAIQLVLGR R NMQSLTFYDAIAQLVLGR R RAVGATFYDQINQLVRKD R SQCRGGFYDAIYQLVTGV R GGSVLSFYDAIDQLVGGG	0E2A-4-E11- 0E2A-3-A4-I 0E2A-4-G8-I 0E2A-3-B7-I 0E2A-4-G11-
R GGDGDPFYDWIEQLVRAG R LDLCASFYDAIEQLVGVK R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLVRGG R RLQPRTFYEAIDQLIGGV R SGAHRTFYDAIQELVGMG R NMQSLTFYDAIAQLVLGR R RAVGATFYDQINQLVRKD R SQCRGGFYDAIYQLVTGV R GNRQRGFYDAIDQLVHCC	0E2A-4-E11- 0E2A-3-A4-I 0E2A-4-G8-I 0E2A-3-B7-I
R GGDGDPFYDWIEQLVRAG R LDLCASFYDAIEQLVGVK R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLVRGG R RLQPRTFYEAIDQLIGGV R SGAHRTFYDAIQELVGMG R NMQSLTFYDAIAQLVLGR IR RAVGATFYDQINQLVRKD R SQCRGGFYDAIYQLVTGV R DRLAFSFYDAIDQLVHCC	0E2A-4-E11- 0E2A-3-A4-I 0E2A-4-G8-I
R GGDGDPFYDWIEQLVRAG R LDLCASFYDAIEQLVGVK R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLVRGG R RLQPRTFYEAIDQLIGGV R SGAHRTFYDAIQELVGMG R NMQSLTFYDAIAQLVLGR IR RAVGATFYDQINQLVRKD R SQCRGGFYDAIYQLVTGV	0E2A-4-EII- 0E2A-3-A4-I
R GGDGDPFYDWIEQLVRAG R LDLCASFYDAIEQLVGVK R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLVRGG R RLQPRTFYEAIDQLIGGV R SGAHRTFYDAIQELVGMG R NMQSLTFYDAIAQLVLGR RAVGATFYDQINQLVRKD	0E2A-4-EII-
R GGDGDPFYDWIEQLVRAG R LDLCASFYDAIEQLVGVK R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLVRGG R RLQPRTFYEAIDQLIGGV R SGAHRTFYDAIQELVGMG R NMQSLTFYDAIAQLVLGR	
R GGDGDPFYDWIEQLVRAG R LDLCASFYDAIEQLVGVK R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLVRGG R RLQPRTFYEAIDQLIGGV R SGAHRTFYDAIQELVGMG	20E2A-4-E5-I
R GGDGDPFYDWIEQLVRAG R LDLCASFYDAIEQLVGVK R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLVRGG R RLQPRTFYEAIDQLIGGV	20E2A-3-D7-I
R GÖDGDPFYDWIEQLVRAG R LDLCASFYDAIEQLVGVK R WLACQSFYDAIDQLINGG R EVNALSFYDAIDQLVRGG	20E2A-4-H9-I
R ĢĞDGDPFYDWIEQL R LDLCASFYDAIEQL R WLACQSFYDAIDQL	20E2A-3-A1-I
R GGDGDPFYDWIEQL R LDLCASFYDAIEQL	20E2A-3-D5-I
R GGDGDPFYDWIEQLVRAGS	20E2A-4-H7-I
12	20E2A-4-F2-I
R AOPCVSFYDAIEQL	20E2A-4-G1-I
R	20E2A-4-H5-I
IR FORTWSFYDAINOLVMEGSG	
IR VS	20E2A-4-H10-
IR RSSCQSFYDAIERLVLGGTCG	-3- <u>B</u> 3-I
XXXXXXFYDAIDQLVXXXXX	Девідп
Sequence	Clone

17.5	23.1	21.3			15.5		12.2	23.2	21.3	21.6	•	24.2	22.9	21.1	-	0	22.5	24.1	24.1	24.0	23.8	22.7	22.6	20.1	21.4	21.3	4.3	24.8	22.4	:	E-Tag	Ratios ov	
17.1	20.7	19.9	19.3	19.1	11.0	5.9	5.7		•			•	23.1	21.4	18.0	17.5	14.6	23.5	w	2	-	1.	1.	0		18.3	2.2	24.5	18.6	:	IGFsR	er Backgro	
12.1	13.6	13.3	13.0	12.8	7.2	3.9				•	9.4	19.0	17.7	16.9	13.8	13.4	11.7	20.9	21.0	20.8	19.9	18.9		•	16.0	16.5	2.1	21.2	15.9	:	₹	und	
1.4	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.2	1.2	1.2	1.2	1.3	1.3	1.3	1.3	1.3	1.3	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.2	1.2	:	<b>IGFIVIR</b>	Compa	
0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	1	IR/IGFR	isons	
	17.1 12.1 1.4	.7 13.6 1.5 .1 12.1 1.4	19.9 13.3 1.5 20.7 13.6 1.5 17.1 12.1 1.4	19.3 13.0 1.5 19.9 13.3 1.5 20.7 13.6 1.5 17.1 12.1 1.4	.2 19.1 12.8 1.5 .8 19.3 13.0 1.5 .3 19.9 13.3 1.5 .1 20.7 13.6 1.5 .5 17.1 12.1 1.4	.5     11.0     7.2     1.5       .2     19.1     12.8     1.5       .8     19.3     13.0     1.5       .3     19.9     13.3     1.5       .1     20.7     13.6     1.5       .5     17.1     12.1     1.4	.9       5.9       3.9       1.5         .5       11.0       7.2       1.5         .2       19.1       12.8       1.5         .8       19.3       13.0       1.5         .3       19.9       13.3       1.5         .1       20.7       13.6       1.5         .5       17.1       12.1       1.4	.2       5.7       3.8       1.5         .9       5.9       3.9       1.5         .5       11.0       7.2       1.5         .2       19.1       12.8       1.5         .8       19.3       13.0       1.5         .3       19.9       13.3       1.5         .1       20.7       13.6       1.5         .5       17.1       12.1       1.4	.2       22.2       18.0       1.2       0.         .2       5.7       3.8       1.5       0.         .9       5.9       3.9       1.5       0.         .5       11.0       7.2       1.5       0.         .2       19.1       12.8       1.5       0.         .8       19.3       13.0       1.5       0.         .3       19.9       13.3       1.5       0.         .1       20.7       13.6       1.5       0.         .5       17.1       12.1       1.4       0.	.3     19.6     16.3     1.2     0.       .2     22.2     18.0     1.2     0.       .2     5.7     3.8     1.5     0.       .9     5.9     3.9     1.5     0.       .5     11.0     7.2     1.5     0.       .2     19.1     12.8     1.5     0.       .8     19.3     13.0     1.5     0.       .3     19.9     13.3     1.5     0.       .1     20.7     13.6     1.5     0.       .5     17.1     12.1     1.4     0.	.6       13.7       11.6       1.2       0.         .3       19.6       16.3       1.2       0.         .2       22.2       18.0       1.2       0.         .2       5.7       3.8       1.5       0.         .9       5.9       3.9       1.5       0.         .5       11.0       7.2       1.5       0.         .2       19.1       12.8       1.5       0.         .8       19.3       13.0       1.5       0.         .3       19.9       13.3       1.5       0.         .1       20.7       13.6       1.5       0.         .5       17.1       12.1       1.4       0.	1     11.5     9.4     1.2     0.       .6     13.7     11.6     1.2     0.       .3     19.6     16.3     1.2     0.       .2     22.2     18.0     1.2     0.       .2     5.7     3.8     1.5     0.       .9     5.9     3.9     1.5     0.       .5     11.0     7.2     1.5     0.       .2     19.1     12.8     1.5     0.       .8     19.3     13.0     1.5     0.       .3     19.9     13.3     1.5     0.       .1     20.7     13.6     1.5     0.       .5     17.1     12.1     1.4     0.	4.2       24.3       19.0       1.3       0.         7.1       11.5       9.4       1.2       0.         1.6       13.7       11.6       1.2       0.         1.3       19.6       16.3       1.2       0.         3.2       22.2       18.0       1.2       0.         2.2       5.7       3.8       1.5       0.         4.9       5.9       3.9       1.5       0.         5.5       11.0       7.2       1.5       0.         2.2       19.1       12.8       1.5       0.         1.8       19.3       13.0       1.5       0.         1.3       19.9       13.3       1.5       0.         7.5       17.1       12.1       1.4       0.	2.9     23.1     17.7     1.3     0.       4.2     24.3     19.0     1.3     0.       7.1     11.5     9.4     1.2     0.       1.6     13.7     11.6     1.2     0.       1.3     19.6     16.3     1.2     0.       3.2     22.2     18.0     1.2     0.       2.2     5.7     3.8     1.5     0.       2.2     5.9     3.9     1.5     0.       5.5     11.0     7.2     1.5     0.       2.2     19.1     12.8     1.5     0.       1.3     19.3     13.0     1.5     0.       1.3     19.9     13.3     1.5     0.       7.5     17.1     12.1     1.4     0.	1.1     21.4     16.9     1.3     0.       2.9     23.1     17.7     1.3     0.       4.2     24.3     19.0     1.3     0.       7.1     11.5     9.4     1.2     0.       1.6     13.7     11.6     1.2     0.       1.3     19.6     16.3     1.2     0.       1.3     19.6     16.3     1.2     0.       2.2     5.7     3.8     1.5     0.       2.2     5.7     3.8     1.5     0.       2.2     5.7     3.8     1.5     0.       2.2     19.0     7.2     1.5     0.       2.2     19.1     12.8     1.5     0.       1.3     19.3     13.0     1.5     0.       1.3     19.9     13.3     1.5     0.       7.5     17.1     12.1     1.4     0.	1.7     18.0     13.8     1.3     0.       1.1     21.4     16.9     1.3     0.       2.9     23.1     17.7     1.3     0.       4.2     24.3     19.0     1.3     0.       7.1     11.5     9.4     1.2     0.       1.6     13.7     11.6     1.2     0.       1.3     19.6     16.3     1.2     0.       3.2     22.2     18.0     1.2     0.       2.2     5.7     3.8     1.5     0.       2.2     5.9     3.9     1.5     0.       5.5     11.0     7.2     1.5     0.       1.8     19.3     13.0     1.5     0.       1.3     19.9     13.3     1.5     0.       7.5     17.1     12.1     1.4     0.	0.2     17.5     13.4     1.3     0.       1.7     18.0     13.8     1.3     0.       1.1     21.4     16.9     1.3     0.       2.9     23.1     17.7     1.3     0.       4.2     24.3     19.0     1.3     0.       7.1     11.5     9.4     1.2     0.       1.6     13.7     11.6     1.2     0.       1.3     19.6     16.3     1.2     0.       1.3     19.6     16.3     1.2     0.       2.2     22.2     18.0     1.2     0.       2.2     5.7     3.8     1.5     0.       2.2     5.9     3.9     1.5     0.       2.2     19.1     12.8     1.5     0.       1.8     19.3     13.0     1.5     0.       1.3     19.9     13.3     1.5     0.       7.5     17.1     12.1     1.4     0.	2.5     14.6     11.7     1.3     0.       0.2     17.5     13.4     1.3     0.       1.7     18.0     13.8     1.3     0.       1.1     21.4     16.9     1.3     0.       2.9     23.1     17.7     1.3     0.       4.2     24.3     19.0     1.3     0.       7.1     11.5     9.4     1.2     0.       1.6     13.7     11.6     1.2     0.       1.3     19.6     16.3     1.2     0.       1.3     19.6     16.3     1.2     0.       2.2     22.2     18.0     1.2     0.       2.2     5.7     3.8     1.5     0.       2.2     5.9     3.9     1.5     0.       2.2     19.1     12.8     1.5     0.       1.8     19.3     13.0     1.5     0.       1.3     19.9     13.3     1.5     0.       7.5     17.1     12.1     1.4     0.	4.1       23.5       20.9       1.1       0.         2.5       14.6       11.7       1.3       0.         1.7       18.0       13.8       1.3       0.         1.1       21.4       16.9       1.3       0.         2.9       23.1       17.7       1.3       0.         4.2       24.3       19.0       1.3       0.         7.1       11.5       9.4       1.2       0.         1.6       13.7       11.6       1.2       0.         1.3       19.6       16.3       1.2       0.         1.3       19.6       16.3       1.2       0.         2.2       22.2       18.0       1.2       0.         2.2       5.7       3.8       1.5       0.         2.2       5.9       3.9       1.5       0.         2.2       19.1       12.8       1.5       0.         1.3       19.9       13.0       1.5       0.         1.3       19.9       13.3       1.5       0.         1.3       19.9       13.3       1.5       0.         1.5       0.       1.5       0.	4.1       23.5       21.0       1.1       0.         4.1       23.5       20.9       1.1       0.         2.5       14.6       11.7       1.3       0.         0.2       17.5       13.4       1.3       0.         1.7       18.0       13.8       1.3       0.         1.1       21.4       16.9       1.3       0.         2.9       23.1       17.7       1.3       0.         4.2       24.3       19.0       1.3       0.         7.1       11.5       9.4       1.2       0.         1.6       13.7       11.6       1.2       0.         1.3       19.6       16.3       1.2       0.         1.3       19.6       16.3       1.2       0.         2.2       5.7       3.8       1.5       0.         2.2       5.7       3.8       1.5       0.         2.2       5.7       3.8       1.5       0.         2.2       19.1       12.8       1.5       0.         1.3       19.3       13.0       1.5       0.         1.3       19.9       13.3       1.5	.0       22.5       20.8       1.1       0.1         .1       23.5       21.0       1.1       0.1         .5       14.6       11.7       1.3       0.1         .2       17.5       13.4       1.3       0.1         .7       18.0       13.8       1.3       0.1         .1       21.4       16.9       1.3       0.1         .9       23.1       17.7       1.3       0.1         .1       11.5       9.4       1.2       0.1         .1       11.5       9.4       1.2       0.1         .1       11.5       11.6       1.2       0.1         .2       22.2       18.0       1.2       0.1         .2       22.2       18.0       1.5       0.1         .2       5.7       3.8       1.5       0.1         .2       11.0       7.2       1.5       0.1         .3       19.3       13.0       1.5       0.1         .3       19.9       13.3       1.5       0.1         .3       19.9       13.3       1.5       0.1         .3       19.9       13.3       1.5 <th>3.8     21.7     19.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       4.1     23.5     20.9     1.1     0.       2.5     14.6     11.7     1.3     0.       10.2     17.5     13.4     1.3     0.       11.7     18.0     13.8     1.3     0.       12.9     23.1     17.7     1.3     0.       2.2     23.1     17.7     1.3     0.       13.1     11.5     9.4     1.2     0.       13.6     13.7     11.6     12.2     0.       13.1     19.6     16.3     1.2     0.       13.2     22.2     18.0     1.2     0.       2.2     5.7     3.8     1.5     0.       2.5     11.0     7.2     1.5     0.       2.5     11.0     7.2     1.5     0.       2.2     19.1     12.8     1.5     0.       2.1     19.3     13.0     1.5     0.       2.1     19.9     13.3     1.5     0.       2.1     19.9     13.3     1.5     0.       2.1<th>2.7     21.3     18.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       4.1     23.5     20.9     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.7     18.0     13.8     1.3     0.       1.1     21.4     16.9     1.3     0.       1.2     23.1     17.7     1.3     0.       2.9     23.1     17.7     1.3     0.       1.6     13.7     11.6     1.2     0.       1.3     19.6     16.3     1.2     0.       1.3     19.6     16.3     1.2     0.       1.3     19.6     16.3     1.2     0.       2.2     5.7     3.8     1.5     0.       2.2     19.1     12.8     1.5     0.       2.2     19.1     12.8     1.5     0.       1.3     19.9     13.3     1.5     0.       2.2     19.1     12.8     1.5     0.       1.3     19.9     13.6     1.5     0.       2.7</th><th>2.6       21.2       18.6       1.1       0.         2.7       21.3       18.9       1.1       0.         3.8       21.7       19.9       1.1       0.         4.0       22.5       20.8       1.1       0.         4.1       23.5       21.0       1.1       0.         2.5       14.6       11.7       1.3       0.         10.2       17.5       13.4       1.3       0.         11.7       18.0       13.8       1.3       0.         12.9       23.1       17.7       1.3       0.         12.9       23.1       17.7       1.3       0.         13.2       24.3       19.0       1.3       0.         13.3       19.6       16.3       1.2       0.         13.3       19.6       16.3       1.2       0.         13.3       1.2       0.       0.         13.4       19.9       3.9       1.5       0.         13.8       19.9       1.5       0.         13.3       1.5       0.         15.5       11.0       7.2       1.5       0.         15.5       &lt;</th><th>0.1       20.5       18.2       1.1       0.         2.6       21.2       18.6       1.1       0.         2.7       21.3       18.9       1.1       0.         3.8       21.7       19.9       1.1       0.         4.0       22.5       20.8       1.1       0.         4.1       23.5       21.0       1.1       0.         2.5       14.6       11.7       1.3       0.         10.2       17.5       13.4       1.3       0.         11.7       18.0       13.8       1.3       0.         11.1       21.4       16.9       1.3       0.         12.9       23.1       17.7       1.3       0.         13.1       19.6       16.9       1.3       0.         13.2       24.3       19.0       1.3       0.         13.3       19.6       16.3       1.2       0.         13.1       19.6       16.3       1.2       0.         13.2       22.2       18.0       1.5       0.         13.3       1.5       0.         15.5       11.0       7.2       1.5       0.</th><th>1.4     18.3     16.0     1.1     0.       0.1     20.5     18.2     1.1     0.       2.6     21.2     18.6     1.1     0.       2.7     21.3     18.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.2     23.1     17.7     1.3     0.       1.3     19.0     1.3     0.       1.4     16.9     1.3     0.       1.5     9.4     1.2     0.       1.6     13.7     11.6     1.2     0.       1.1     1.5     9.4     1.2     0.       1.3     19.6     16.3     1.2     0.       1.5     1.5     0.     0.       1.5     1.5     0.       1.5     0.     0.       1.5     0.     0.</th><th>1.3     18.3     16.5     1.1     0.1       1.4     18.3     16.0     1.1     0.       2.6     21.2     18.6     1.1     0.       2.7     21.3     18.9     1.1     0.       3.8     21.7     19.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       4.1     23.5     20.9     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.2     23.1     17.7     1.3     0.       1.3     19.0     1.3     0.       1.4     16.9     1.3     0.       1.5     9.4     1.2     0.       1.1     13.7     11.6     1.2     0.       1.1     1.6     1.2     0.       1.2     1.2     1.5     0.       2.2     1.1     1.5     0.       2.3     1.2     1.5     0.       2.1     1.2     1.5&lt;</th><th>4.3     2.2     2.1     1.1     0.1       1.4     18.3     16.5     1.1     0.1       0.1     20.5     18.2     1.1     0.1       2.6     21.2     18.6     1.1     0.1       2.7     21.3     18.9     1.1     0.1       4.0     22.5     20.8     1.1     0.1       4.1     23.5     21.0     1.1     0.1       4.1     23.5     20.9     1.1     0.1       1.7     18.0     11.7     1.3     0.1       1.7     18.0     13.4     1.3     0.1       1.1     21.4     16.9     1.3     0.1       1.1     21.4     16.9     1.3     0.1       1.1     21.4     16.9     1.3     0.1       1.2     23.1     17.7     1.3     0.1       1.3     19.0     1.3     0.1       1.3     19.6     16.3     1.2     0.1       1.4     9     5.9     3.9     1.5     0.1       2.2     19.1     12.8     1.5     0.1       2.3     19.3     13.0     1.5     0.1       2.5     11.0     7.2     1.5     0.1       &lt;</th><th>4.8     24.5     21.2     1.2     0.       1.3     18.3     16.5     1.1     0.       1.4     18.3     16.0     1.1     0.       2.6     21.2     18.6     1.1     0.       2.7     21.3     18.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       4.1     23.5     20.9     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.7     18.0     13.4     1.3     0.       1.7     18.0     13.8     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     11.5     9.4     1.2     0.       1.1     11.5     9.4     1.2     0.       1.1     11.5     1.2     0.       1.2     1.3     1.5     0.       2.     2.7     3.8     1.5     0.       2.     1.1     1.2     1</th><th>2.4       18.6       15.9       1.2       0.         4.8       24.5       21.2       1.1       0.         1.1       18.3       16.5       1.1       0.         0.1       18.3       16.0       1.1       0.         2.6       21.2       18.6       1.1       0.         2.7       21.3       18.9       1.1       0.         2.7       21.3       18.9       1.1       0.         4.0       22.5       20.8       1.1       0.         4.1       23.5       21.0       1.1       0.         4.1       23.5       21.0       1.1       0.         4.1       23.5       21.0       1.1       0.         2.5       14.6       11.7       1.3       0.         1.7       18.0       13.4       1.3       0.         1.1       21.4       16.9       1.3       0.         1.1       21.4       16.9       1.3       0.         1.1       1.5       9.4       1.3       0.         1.3       1.5       1.3       0.         2.2       1.3       1.2       0.</th><th>2.4 18.6 15.9 1.2 0.4 1.3 2.2 2.1 1.1 0.1 1.1 0.2 1.2 1.2 1.2 0.1 1.4 18.3 16.5 18.2 1.1 0.1 1.1 0.2 1.2 1.2 1.2 1.2 1.3 18.5 18.6 1.1 0.2 1.3 18.9 1.1 0.1 1.1 1</th><th>Fag IGESR IR  2.4 18.6 15.9 4.8 24.5 21.2 4.3 2.2 2.1 1.3 18.3 16.0 0.1 20.5 18.2 2.6 21.2 18.6 2.7 21.3 18.9 3.8 21.7 19.9 4.0 22.5 20.8 4.1 23.5 21.0 2.5 14.6 11.7 18.0 13.4 1.1 21.4 16.9 2.9 23.1 17.5 13.4 11.6 13.7 11.6 11.3 19.6 16.3 2.2 24.3 19.0 2.1 3.9 3.9 5.5 11.0 7.2 19.1 12.8 19.3 13.0 13.3 19.9 13.3 19.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 13.6 13.8 19.3 13.0 13.8 19.3 13.0</th><th>Frag         IGFsR         IR         IGFsR         IR         IGFW/IR IR/IGF           2.4         18.6         15.9         1.2         0.4           4.8         24.5         21.2         1.1         0.1           1.4         18.3         16.5         1.1         0.1           2.6         21.2         18.6         1.1         0.1           2.7         21.3         18.9         1.1         0.2           2.7         21.3         18.9         1.1         0.2           2.7         21.3         18.9         1.1         0.2           2.7         21.3         18.9         1.1         0.2           3.8         21.7         19.9         1.1         0.2           4.0         22.5         20.8         1.1         0.2           4.1         23.5         21.0         1.1         0.2           4.1         23.5         21.0         1.1         0.2           1.7         18.0         11.7         1.3         0.1           1.7         18.0         13.8         1.3         0.1           1.1         21.5         9.4         1.2         0.1     <!--</th--></th></th>	3.8     21.7     19.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       4.1     23.5     20.9     1.1     0.       2.5     14.6     11.7     1.3     0.       10.2     17.5     13.4     1.3     0.       11.7     18.0     13.8     1.3     0.       12.9     23.1     17.7     1.3     0.       2.2     23.1     17.7     1.3     0.       13.1     11.5     9.4     1.2     0.       13.6     13.7     11.6     12.2     0.       13.1     19.6     16.3     1.2     0.       13.2     22.2     18.0     1.2     0.       2.2     5.7     3.8     1.5     0.       2.5     11.0     7.2     1.5     0.       2.5     11.0     7.2     1.5     0.       2.2     19.1     12.8     1.5     0.       2.1     19.3     13.0     1.5     0.       2.1     19.9     13.3     1.5     0.       2.1     19.9     13.3     1.5     0.       2.1 <th>2.7     21.3     18.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       4.1     23.5     20.9     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.7     18.0     13.8     1.3     0.       1.1     21.4     16.9     1.3     0.       1.2     23.1     17.7     1.3     0.       2.9     23.1     17.7     1.3     0.       1.6     13.7     11.6     1.2     0.       1.3     19.6     16.3     1.2     0.       1.3     19.6     16.3     1.2     0.       1.3     19.6     16.3     1.2     0.       2.2     5.7     3.8     1.5     0.       2.2     19.1     12.8     1.5     0.       2.2     19.1     12.8     1.5     0.       1.3     19.9     13.3     1.5     0.       2.2     19.1     12.8     1.5     0.       1.3     19.9     13.6     1.5     0.       2.7</th> <th>2.6       21.2       18.6       1.1       0.         2.7       21.3       18.9       1.1       0.         3.8       21.7       19.9       1.1       0.         4.0       22.5       20.8       1.1       0.         4.1       23.5       21.0       1.1       0.         2.5       14.6       11.7       1.3       0.         10.2       17.5       13.4       1.3       0.         11.7       18.0       13.8       1.3       0.         12.9       23.1       17.7       1.3       0.         12.9       23.1       17.7       1.3       0.         13.2       24.3       19.0       1.3       0.         13.3       19.6       16.3       1.2       0.         13.3       19.6       16.3       1.2       0.         13.3       1.2       0.       0.         13.4       19.9       3.9       1.5       0.         13.8       19.9       1.5       0.         13.3       1.5       0.         15.5       11.0       7.2       1.5       0.         15.5       &lt;</th> <th>0.1       20.5       18.2       1.1       0.         2.6       21.2       18.6       1.1       0.         2.7       21.3       18.9       1.1       0.         3.8       21.7       19.9       1.1       0.         4.0       22.5       20.8       1.1       0.         4.1       23.5       21.0       1.1       0.         2.5       14.6       11.7       1.3       0.         10.2       17.5       13.4       1.3       0.         11.7       18.0       13.8       1.3       0.         11.1       21.4       16.9       1.3       0.         12.9       23.1       17.7       1.3       0.         13.1       19.6       16.9       1.3       0.         13.2       24.3       19.0       1.3       0.         13.3       19.6       16.3       1.2       0.         13.1       19.6       16.3       1.2       0.         13.2       22.2       18.0       1.5       0.         13.3       1.5       0.         15.5       11.0       7.2       1.5       0.</th> <th>1.4     18.3     16.0     1.1     0.       0.1     20.5     18.2     1.1     0.       2.6     21.2     18.6     1.1     0.       2.7     21.3     18.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.2     23.1     17.7     1.3     0.       1.3     19.0     1.3     0.       1.4     16.9     1.3     0.       1.5     9.4     1.2     0.       1.6     13.7     11.6     1.2     0.       1.1     1.5     9.4     1.2     0.       1.3     19.6     16.3     1.2     0.       1.5     1.5     0.     0.       1.5     1.5     0.       1.5     0.     0.       1.5     0.     0.</th> <th>1.3     18.3     16.5     1.1     0.1       1.4     18.3     16.0     1.1     0.       2.6     21.2     18.6     1.1     0.       2.7     21.3     18.9     1.1     0.       3.8     21.7     19.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       4.1     23.5     20.9     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.2     23.1     17.7     1.3     0.       1.3     19.0     1.3     0.       1.4     16.9     1.3     0.       1.5     9.4     1.2     0.       1.1     13.7     11.6     1.2     0.       1.1     1.6     1.2     0.       1.2     1.2     1.5     0.       2.2     1.1     1.5     0.       2.3     1.2     1.5     0.       2.1     1.2     1.5&lt;</th> <th>4.3     2.2     2.1     1.1     0.1       1.4     18.3     16.5     1.1     0.1       0.1     20.5     18.2     1.1     0.1       2.6     21.2     18.6     1.1     0.1       2.7     21.3     18.9     1.1     0.1       4.0     22.5     20.8     1.1     0.1       4.1     23.5     21.0     1.1     0.1       4.1     23.5     20.9     1.1     0.1       1.7     18.0     11.7     1.3     0.1       1.7     18.0     13.4     1.3     0.1       1.1     21.4     16.9     1.3     0.1       1.1     21.4     16.9     1.3     0.1       1.1     21.4     16.9     1.3     0.1       1.2     23.1     17.7     1.3     0.1       1.3     19.0     1.3     0.1       1.3     19.6     16.3     1.2     0.1       1.4     9     5.9     3.9     1.5     0.1       2.2     19.1     12.8     1.5     0.1       2.3     19.3     13.0     1.5     0.1       2.5     11.0     7.2     1.5     0.1       &lt;</th> <th>4.8     24.5     21.2     1.2     0.       1.3     18.3     16.5     1.1     0.       1.4     18.3     16.0     1.1     0.       2.6     21.2     18.6     1.1     0.       2.7     21.3     18.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       4.1     23.5     20.9     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.7     18.0     13.4     1.3     0.       1.7     18.0     13.8     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     11.5     9.4     1.2     0.       1.1     11.5     9.4     1.2     0.       1.1     11.5     1.2     0.       1.2     1.3     1.5     0.       2.     2.7     3.8     1.5     0.       2.     1.1     1.2     1</th> <th>2.4       18.6       15.9       1.2       0.         4.8       24.5       21.2       1.1       0.         1.1       18.3       16.5       1.1       0.         0.1       18.3       16.0       1.1       0.         2.6       21.2       18.6       1.1       0.         2.7       21.3       18.9       1.1       0.         2.7       21.3       18.9       1.1       0.         4.0       22.5       20.8       1.1       0.         4.1       23.5       21.0       1.1       0.         4.1       23.5       21.0       1.1       0.         4.1       23.5       21.0       1.1       0.         2.5       14.6       11.7       1.3       0.         1.7       18.0       13.4       1.3       0.         1.1       21.4       16.9       1.3       0.         1.1       21.4       16.9       1.3       0.         1.1       1.5       9.4       1.3       0.         1.3       1.5       1.3       0.         2.2       1.3       1.2       0.</th> <th>2.4 18.6 15.9 1.2 0.4 1.3 2.2 2.1 1.1 0.1 1.1 0.2 1.2 1.2 1.2 0.1 1.4 18.3 16.5 18.2 1.1 0.1 1.1 0.2 1.2 1.2 1.2 1.2 1.3 18.5 18.6 1.1 0.2 1.3 18.9 1.1 0.1 1.1 1</th> <th>Fag IGESR IR  2.4 18.6 15.9 4.8 24.5 21.2 4.3 2.2 2.1 1.3 18.3 16.0 0.1 20.5 18.2 2.6 21.2 18.6 2.7 21.3 18.9 3.8 21.7 19.9 4.0 22.5 20.8 4.1 23.5 21.0 2.5 14.6 11.7 18.0 13.4 1.1 21.4 16.9 2.9 23.1 17.5 13.4 11.6 13.7 11.6 11.3 19.6 16.3 2.2 24.3 19.0 2.1 3.9 3.9 5.5 11.0 7.2 19.1 12.8 19.3 13.0 13.3 19.9 13.3 19.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 13.6 13.8 19.3 13.0 13.8 19.3 13.0</th> <th>Frag         IGFsR         IR         IGFsR         IR         IGFW/IR IR/IGF           2.4         18.6         15.9         1.2         0.4           4.8         24.5         21.2         1.1         0.1           1.4         18.3         16.5         1.1         0.1           2.6         21.2         18.6         1.1         0.1           2.7         21.3         18.9         1.1         0.2           2.7         21.3         18.9         1.1         0.2           2.7         21.3         18.9         1.1         0.2           2.7         21.3         18.9         1.1         0.2           3.8         21.7         19.9         1.1         0.2           4.0         22.5         20.8         1.1         0.2           4.1         23.5         21.0         1.1         0.2           4.1         23.5         21.0         1.1         0.2           1.7         18.0         11.7         1.3         0.1           1.7         18.0         13.8         1.3         0.1           1.1         21.5         9.4         1.2         0.1     <!--</th--></th>	2.7     21.3     18.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       4.1     23.5     20.9     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.7     18.0     13.8     1.3     0.       1.1     21.4     16.9     1.3     0.       1.2     23.1     17.7     1.3     0.       2.9     23.1     17.7     1.3     0.       1.6     13.7     11.6     1.2     0.       1.3     19.6     16.3     1.2     0.       1.3     19.6     16.3     1.2     0.       1.3     19.6     16.3     1.2     0.       2.2     5.7     3.8     1.5     0.       2.2     19.1     12.8     1.5     0.       2.2     19.1     12.8     1.5     0.       1.3     19.9     13.3     1.5     0.       2.2     19.1     12.8     1.5     0.       1.3     19.9     13.6     1.5     0.       2.7	2.6       21.2       18.6       1.1       0.         2.7       21.3       18.9       1.1       0.         3.8       21.7       19.9       1.1       0.         4.0       22.5       20.8       1.1       0.         4.1       23.5       21.0       1.1       0.         2.5       14.6       11.7       1.3       0.         10.2       17.5       13.4       1.3       0.         11.7       18.0       13.8       1.3       0.         12.9       23.1       17.7       1.3       0.         12.9       23.1       17.7       1.3       0.         13.2       24.3       19.0       1.3       0.         13.3       19.6       16.3       1.2       0.         13.3       19.6       16.3       1.2       0.         13.3       1.2       0.       0.         13.4       19.9       3.9       1.5       0.         13.8       19.9       1.5       0.         13.3       1.5       0.         15.5       11.0       7.2       1.5       0.         15.5       <	0.1       20.5       18.2       1.1       0.         2.6       21.2       18.6       1.1       0.         2.7       21.3       18.9       1.1       0.         3.8       21.7       19.9       1.1       0.         4.0       22.5       20.8       1.1       0.         4.1       23.5       21.0       1.1       0.         2.5       14.6       11.7       1.3       0.         10.2       17.5       13.4       1.3       0.         11.7       18.0       13.8       1.3       0.         11.1       21.4       16.9       1.3       0.         12.9       23.1       17.7       1.3       0.         13.1       19.6       16.9       1.3       0.         13.2       24.3       19.0       1.3       0.         13.3       19.6       16.3       1.2       0.         13.1       19.6       16.3       1.2       0.         13.2       22.2       18.0       1.5       0.         13.3       1.5       0.         15.5       11.0       7.2       1.5       0.	1.4     18.3     16.0     1.1     0.       0.1     20.5     18.2     1.1     0.       2.6     21.2     18.6     1.1     0.       2.7     21.3     18.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.2     23.1     17.7     1.3     0.       1.3     19.0     1.3     0.       1.4     16.9     1.3     0.       1.5     9.4     1.2     0.       1.6     13.7     11.6     1.2     0.       1.1     1.5     9.4     1.2     0.       1.3     19.6     16.3     1.2     0.       1.5     1.5     0.     0.       1.5     1.5     0.       1.5     0.     0.       1.5     0.     0.	1.3     18.3     16.5     1.1     0.1       1.4     18.3     16.0     1.1     0.       2.6     21.2     18.6     1.1     0.       2.7     21.3     18.9     1.1     0.       3.8     21.7     19.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       4.1     23.5     20.9     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.2     23.1     17.7     1.3     0.       1.3     19.0     1.3     0.       1.4     16.9     1.3     0.       1.5     9.4     1.2     0.       1.1     13.7     11.6     1.2     0.       1.1     1.6     1.2     0.       1.2     1.2     1.5     0.       2.2     1.1     1.5     0.       2.3     1.2     1.5     0.       2.1     1.2     1.5<	4.3     2.2     2.1     1.1     0.1       1.4     18.3     16.5     1.1     0.1       0.1     20.5     18.2     1.1     0.1       2.6     21.2     18.6     1.1     0.1       2.7     21.3     18.9     1.1     0.1       4.0     22.5     20.8     1.1     0.1       4.1     23.5     21.0     1.1     0.1       4.1     23.5     20.9     1.1     0.1       1.7     18.0     11.7     1.3     0.1       1.7     18.0     13.4     1.3     0.1       1.1     21.4     16.9     1.3     0.1       1.1     21.4     16.9     1.3     0.1       1.1     21.4     16.9     1.3     0.1       1.2     23.1     17.7     1.3     0.1       1.3     19.0     1.3     0.1       1.3     19.6     16.3     1.2     0.1       1.4     9     5.9     3.9     1.5     0.1       2.2     19.1     12.8     1.5     0.1       2.3     19.3     13.0     1.5     0.1       2.5     11.0     7.2     1.5     0.1       <	4.8     24.5     21.2     1.2     0.       1.3     18.3     16.5     1.1     0.       1.4     18.3     16.0     1.1     0.       2.6     21.2     18.6     1.1     0.       2.7     21.3     18.9     1.1     0.       4.0     22.5     20.8     1.1     0.       4.1     23.5     21.0     1.1     0.       4.1     23.5     20.9     1.1     0.       2.5     14.6     11.7     1.3     0.       1.7     18.0     13.4     1.3     0.       1.7     18.0     13.4     1.3     0.       1.7     18.0     13.8     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     21.4     16.9     1.3     0.       1.1     11.5     9.4     1.2     0.       1.1     11.5     9.4     1.2     0.       1.1     11.5     1.2     0.       1.2     1.3     1.5     0.       2.     2.7     3.8     1.5     0.       2.     1.1     1.2     1	2.4       18.6       15.9       1.2       0.         4.8       24.5       21.2       1.1       0.         1.1       18.3       16.5       1.1       0.         0.1       18.3       16.0       1.1       0.         2.6       21.2       18.6       1.1       0.         2.7       21.3       18.9       1.1       0.         2.7       21.3       18.9       1.1       0.         4.0       22.5       20.8       1.1       0.         4.1       23.5       21.0       1.1       0.         4.1       23.5       21.0       1.1       0.         4.1       23.5       21.0       1.1       0.         2.5       14.6       11.7       1.3       0.         1.7       18.0       13.4       1.3       0.         1.1       21.4       16.9       1.3       0.         1.1       21.4       16.9       1.3       0.         1.1       1.5       9.4       1.3       0.         1.3       1.5       1.3       0.         2.2       1.3       1.2       0.	2.4 18.6 15.9 1.2 0.4 1.3 2.2 2.1 1.1 0.1 1.1 0.2 1.2 1.2 1.2 0.1 1.4 18.3 16.5 18.2 1.1 0.1 1.1 0.2 1.2 1.2 1.2 1.2 1.3 18.5 18.6 1.1 0.2 1.3 18.9 1.1 0.1 1.1 1	Fag IGESR IR  2.4 18.6 15.9 4.8 24.5 21.2 4.3 2.2 2.1 1.3 18.3 16.0 0.1 20.5 18.2 2.6 21.2 18.6 2.7 21.3 18.9 3.8 21.7 19.9 4.0 22.5 20.8 4.1 23.5 21.0 2.5 14.6 11.7 18.0 13.4 1.1 21.4 16.9 2.9 23.1 17.5 13.4 11.6 13.7 11.6 11.3 19.6 16.3 2.2 24.3 19.0 2.1 3.9 3.9 5.5 11.0 7.2 19.1 12.8 19.3 13.0 13.3 19.9 13.3 19.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 11.6 13.7 13.6 13.8 19.3 13.0 13.8 19.3 13.0	Frag         IGFsR         IR         IGFsR         IR         IGFW/IR IR/IGF           2.4         18.6         15.9         1.2         0.4           4.8         24.5         21.2         1.1         0.1           1.4         18.3         16.5         1.1         0.1           2.6         21.2         18.6         1.1         0.1           2.7         21.3         18.9         1.1         0.2           2.7         21.3         18.9         1.1         0.2           2.7         21.3         18.9         1.1         0.2           2.7         21.3         18.9         1.1         0.2           3.8         21.7         19.9         1.1         0.2           4.0         22.5         20.8         1.1         0.2           4.1         23.5         21.0         1.1         0.2           4.1         23.5         21.0         1.1         0.2           1.7         18.0         11.7         1.3         0.1           1.7         18.0         13.8         1.3         0.1           1.1         21.5         9.4         1.2         0.1 </th

FIGURE 2L (Con't)



20E2A-3-D9-IR 20E2A-3-B5-IR 20E2A-3-A6-IR 20E2A-4-G12-IR	-3-C12 -3-A2- -3-C7-	-4-E10 -3-D2- -4-F1- -3-D1-	20E2A-4-G2-IR 20E2A-3-A9-IR 20E2A-3-D3-IR 20E2A-3-A11-IR 20E2A-3-B4-IR	Clone Design 20E2A-3-C2-IR 20E2A-3-B1-IR 20E2A-3-A8-IR
KQRGVTFYDLLNQLVGGSARG PRAPRSFYDAIHQLVGRQGPG PCSDDQFYDALSQLVGIRVCP SYGYQSFYDAIEELVRGPPAR	RPLRWSFYDALDQLVGSAIGG MQGRGGFYDAIADLVGGHVRG TSQGLSFYDAINQLVAGGWGG SGGTVTFYDAINQLVQGRYNG GGALDPFYDAIYQLVIRGSSG	IYTGQGFYDAIEQLVRGGSTP KSPALSFYDAIEQLVGSQGVR ISPPWTFYDAIDQLVGGSDGR GSRFRGFYDAIDQLVRQGGLE GVAGGTFYDAIEQLVRQFGGS	IRSVFSFYDAIDQLVGKGGWS GGVSLTFYEAIEQLVRGGFDA AAQAFSFYDLINQLVASKPSE QSGACGFYDAINQLVLGVSIC GGIVFSFYEAIDQLVRGNGAG	Sequence xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

9.0	17.8	4.				18.9		w •	0	9	4	2.	22.3	۲.	į.	24.4		18.9		22.1	23.4	:	Ratios ov E-Tag
9.3	•	18.1			•		23.0			•	•	•	9.	•	•	24.5	•	•	4.8	21.6	20.9	:	er Backgro IGFsR
2.6	_					7.5							11.3			13.5	11.3					:	und IR
•	2.5	•	•	•	•	1.5	1.6	1.6	1.6	1.6	1.6	1.7	1.7	1.7	1.7	1.8	1.8	1.8	1.8	1.4	1.4	:	Compa IGFR/IR
	0.4							•	•	•	•	•	•	•	0.6	0.6	0.6	•	•	•	0.7	;	risons IR/IGFR



E2A-4-H5-IGFR	20E2A-3-B11-IGFR 20E2A-3-D12-IGFR 20E2A-4-H11-IGFR	E2A-3-A9-IGF E2A-3-A10-IG	0E2A-4-H1-IGF 0E2A-4-F7-IGF 0E2A-3-D7-IGF	0E2A-3-D10 0E2A-3-A12 0E2A-3-A11	20E2A-4-F3-IGFR 20E2A-3-B2-IGFR 20E2A-4-G8-IGFR	0E2A-4-F6-IGF 0E2A-3-A8-IGF 0E2A-4-F9-IGF	20E2A-4-F4-IGFR 20E2A-3-C7-IGFR 20E2A-3-C10-IGFR 20E2A-3-D6-IGFR	June lesign larental 1052A-4-F11-IG 1052A-4-F12-IG 1052A-3-B4-IGF
RWAFQSFYDAIDHLVNHREGH LPPSSGFYNAIQQLVCGHRGC	GRSLLSFYDLIDQLVQAGNGG GQRAQSFYEALARLVCEGRCT CREOGSEYDAIDLLVLGVBTC	VSMPQSFYDALKQLVRGISEG IGVSRGFYDAIDKLVRDRGSP	PSGFLSFYEAIDQLVHGVRWF AFTPTSFYDAIEQLVQQLSPR VSSI.PSSFYDAIDGLVBBBBCO	MMVVDGFYDALHQLVVAQSLG LSVALSFYDALGQLVAGEGRW	VGSSSFYEAIERLVOGLGRH LSWAAGFYEAIDOLVRSGGHR OOVHAGFYEALEELVGFGFLG	LRSQLSFYEAIDQLVQWKGGA DKFFTSFYDAIDQLVQSVRGV MQSGFSFYDAIDRLVGRLGER	YSDTYSFYDAIVQLVRRGASA VGTVAGFYDAIAQLVARASRV RFVWGSFYDAIDQLVQGRWRG RAVGDSFYFAIOOLVBGGHGV	EYDAIDQLVXXXX QLVRGSÅRAGGTRD FYDAIDRLLRMRIG FYDAIDQLLRRRGG

E-Tag 30.6 21.3 23.3 21.8	0.		5		2	, <u>-</u>	20.6 18.7	0					9	•		•	15.8	•	2	•	21.0
113 R	20.0		11.8	19.9			19.3 14.7				•		•	•	•	•		•	•		
1R 4.2 1.3 3.1 2.4		4.2		•	•	•	ა <u>4</u> 8	•	•		2.6		5. <sub>3</sub>	•		4.8	υ • •	2.8	5.7	5.5	4.2
.6 .8	5.5 5.1	5.0		•	•	•	ս 4 9 2		•		•	•	•			. w . N	3.2	3.2	3.1	3.0	3.0
	0.2	0.2	•	0.2		•	0.2			•		•		•	•		0.3		•		0.3



24.	<b>5</b> .	16.	17.	22.	23.	25.	26.	23.	19.	22.	20.	23.	N	22.	$\vdash$	24.	22.	23.	21.	22.	21.	19.	•	25.	20.	15.	18.	24.	16.	19.	:	E-Tag	Ratio
4.	2	1	2	O	_	ω	.4	.0	. 6	6	ū	0	6	w	ω	w	.2	G	0	6	4	80	σ	. 9	7	_	_	0	_	4		,·	s over
21.1	3.0	6.1	8.6	17.7	17.9	20.7	22.1	17.1	19.9	14.5	15.7	16.6	19.9	22.6	2.7	16.3	17.1	17.4	21.8	21.3	21.6	12.3	14.6	17.4	ພ . ພ	9.3	20.6	14.3	11.8	19.0	•	GFSR	Ratios over Background
11.5	1.5	3.2	4.6	9.3	9.5	11.1	11.5	8.7	9.8	7.0	7.6	7.9	9.4	10.8	1.2	7.4	7.7	7.8	10.1	9.1	9.3	5.1	6.0	7.2	1.3	3.6	7.9	5.3	4.2	6.8	:	₹	μφ
1.8	1.9	1.9	1.9	1.9	1.9	1.9	1.9	2.0	2.0	2.1	2.1	2.1	2.1	2.1	2.2	2.2			2.2		2.3	2.4	2.4	2.4	2.6	2.6	2.6	2.7	. 2.8	2.8	;	ICFIVIR	Comparisons
0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.4	0.4	0.5	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	:	IR/IGER	risons

FIGURE 2M (Con't)



20E2A-3-A5 20E2A-3-C1	20E2A-4-H8	20E2A-3-C2	20E2A-4-F5	20E2A-4-G6	20E2A-4-E8	20E2A-3-D2	20E2A-3-C6	20E2A-3-D1	20E2A-4-E1	20E2A-3-A7	20E2A-3-A4	20E2A-4-G1	20E2A-4-H9	20E2A-4-H6	20E2A-4-G9	20E2A-3-B6	20E2A-4-H2	-3 -C	-4-H1	20E2A-3-C8	20E2A-3-B8	0E2A-3-B1	0E2A-4-H1	20E2A-3-A6	20E2A-4-F8	20E2A-4-H4	20E2A-3-B5	20E2A-4-G3	20E2A-4-G2	Design	Clone
- IGFR	- IGFR	- IGFR	- IGFR	- IGFR	- IGFR I	- IGFR C	- IGFR E		2-IGFR 1	- IGFR E	- IGFR	0-IGFR F	- IGFR	-IGFR H	- IGFR S	-IGFR E	- IGFR F	-IGFR W	0-IGFR P	- IGFR L	- IGFR T	2-IGFR V	2-IGFR F	- IGFR F	-IGFR V	- IGFR S	- IGFR "V	- IGFR F	- IGFR 1	Ų	
TPGGFSFYDAIQQLVDVLSDS TNAALTFYDAIEQLVRWGQRD	VRGFYEAI		LVTGGW	HGEKLSFYÞAIAQLVGFDIGH	AGPDMSFYDAIDQLVHCCGPF	LVGGE	<b>PVVLFSFYDAIDQLVRKGLGP</b>		LGRADGFYDAIKQLVGADWGG	PRESFSFYDAIHQLVTGRVRS	AGSVTSFYDAMEQLVATGTSA	FTSFHTFYDAIEQLVGQGGDP	GRGWGSFYEAIDQLVRGLGET	KFRVYTFYDAIDQLVNQGRGR	SVGPRSFYDAIDQLVGGAWVG	EDQPNSFYDA I RQLVMGRLSP	<b>FAFVGSFYDALAQLVAQGPRS</b>	WDLVDSFYDAIDQLVGQRVPG	ASSRLSFYDA I EQL I KWSPGP		TTYVNSFYDALQQLLGGDADV	VMRRDRFYDAIEQLVGGRIGV	PVSATSFYDAINQLVRMGSRG	PSPVWSFYDAI <u>Q</u> QLVRSGQRG	VGAAFSFYDAIDQLVGWSPGS	<u>Q</u> VFRGSFYDAIDALVRWGGRA	VRQAKSFYDA I DQLVRGALRG	RDVADGFYAA I EQLVRGQFGL	IGVLGSFYDA IDQLVRQGGNR	XXXXXXFYDAIDQLVXXXXX	Sequence

								•																									
	22.7	24.4	22.5	21.7	24.7	18.4	21.4	23.7	24.0	23.3	26.0	6.	25.3	4.	21.9	26.0	20.3	21.8	S	25.3	w	$\vdash$	27.6	5	23.8	17.3	22.2	24.0	21.2	22.3	:	E-Tag	Ratios ov
24.3	15.6	18.5	19.6	21.7		13.6	15.1	21.7	22.4	23.1	24.9	•		16.8	٠	16.1	18.1	20.1	21.8	23.8	17.7	19.0	21.9		23.7	17.9	20.6	22.7	12.3	17.5	1	IGFsR	Ratios over Background
21.2	12.6	15.1	15.8	18.2	17.7	10.4	11.4	17.2	17.6	17.8	19.3	1.8		11.8	•	10.8	11.8	13.0	14.6	16.2		12.2	13.6	14.2	15.0	10.7	12.0	13.3	6.9	9.9	:	R	puń
1.1	1.2	1.2	1.2	1.2	1.2	1.3	1.3	1.3	1.3	1.3	1.3	1.4	1.4	1.4	1.4	1.5	1.5	1.5	1.5	1.5	1.6	1.6	1.6	1.6	1.6	1.7	1.7	1.7	1.8	1.8	;	IGFIVIR	Compa
0.9	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.7	0.7	0.7	0.7	0.7	0.7	0.6	0.7	0.7	0.6	0.6	0.6	0.6	<b>0.6</b>	0.6	0.6	0.6	0.6	0.6	:	IR/IGER	risons

FIGURE 2M (Con't)



20E2A-3-¤8-IGFR	20E2A-3-B3-IGFR	20E2A-3-C1-IGFR	Design	Clone
SAGPLSFYDAIAQLVGPAWRL	AGQLGGFYIAICQLVGYEYCT	GQSPLSFYDAIDQLVRAFPVG	XXXXXXFYDAIDQLVXXXXXX	Sequence

Ratios ov	E-Tag	;	23.4	21.0	
Ratios over Background	IGESR	:	22.4	17.0	
ų nd	R	1	20.5	14.8	,
Comparisons	IÇFIVIR IR/IGFR	!	1.1	1.1	
risons	IR/IGFR	:	0.9	0.9	



20E2Bα-4-H7-IR S		20E2Bα-4-H11-IR W	20E2Bα-4-F11-IR Q	20E2Bα-4-E10-IR D	20E2Bα-4-G11-IR W	20E2Bα-4-G1-IR Q	20E2Bα-3-B5-IR F	20E2Bα-3-B7-IR A	20E2Bα-3-A11-IR R	20E2Bα-3-B12-IR I	20E2Bα-4-F7-IR V	20E2Bα-3-D5-IR A	20E2Bα-4-E7-IR L	20E2Bα-4-F9-IR A	20E2Bα-4-G8-IR A	20E2Bα-4-E9-IR C	20E2Bα-3-A3-IR L	20E2Bα-3-A5-IR F	20E2Bα-3-D2-IR V	20E2Bα-3-B8-IR	20E2Bα-4-F12-IR S	20E2Bα-3-B3-IR	al	gn	Clone
SSGCQDFYSCMIQLVTGGGGD	QTVHRDFYAALQDLLINDLGF	WSGNVDFYYMIRQLCGDVCGS	QHSCRTFYDCIRVLMDDGQLG	DSTVCGFYCRLAQLVAEGGSP	WGLRDDFYRGIRCLVQWSEGC	QKRSEAFYDWIADLLGQETSG	PGGGEGFYQGLQRL1LGADGG	<b>AQRCADFYACIEELLAPGSWR</b>	RAGSRGFYEFFENLLRVGAGG	IRGADQFYQFFRELLEGSVGE	VQACQNFYDCLNTLLLLDLGG	<b>ATCASSFYAQLNCLLSDFDVM</b>	LARNDEFYRYFEQLVFGDTEG	<b>AVHEDGFYDMLRKLLSEGDSS</b>	<b>ACEGGSFYGCLQSLMSVESGN</b>	CKDQPDFYMGIKCLISGGGSV	DLGGNSFYYGLLRLVLQDAVG	RNYPIGFYQFFHELVISSGGG	<b>VQCRADFYSYFACLVGRPGSR</b>	IEVTQPFYDYFQQLLRLYGND	SVKEVQFYRYFYDLLQSEESG	AGVNAGFYRYFSTLLDWWDQG	FYDAIDQLVRGSARAGGTRD	XXXXXFYXXhXXhhXXXXXX	Sequence

<u>ب</u>	38.7	34.8	32.5	35.4	33.2	38.5	41.6	40.4	36.9	37.0	36.6	39.5	36.0	35.6	37.5	32.8	39.9	36.9	42.6	39.3	35.5	33.5	30.6	;	E-Tag	Datine Ov
•	34.9	32.0	29.5	30.5	30.1	28.9	36.4	37.1	34.9	33.4	32.9	33.1	31.6	32.5	30.5	29.6	33.5	22.7	19.7	18.2	5.9	1.2	15.1	•	E-Tag IGFsR II	ar Rackorn
	30.5	28.7	_	28.0	27.8	26.5	34.5	36.3	34.2	33.5	32.5	31.8	31.2	31.1	30.9	28.6	35.5	24.5	26.7	36.5	27.8	23.5	4.2	;	SHI SHI	
1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.9	0.9	φ.7	0.5	0.2	0.1	3.6	:	ICER/IR	Compa
0.9	0.9	0.9	0.9	0.9	0.9	0.9	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.1	1.1	1.4	2.0	4.7	20.0	0.3	:	GFR/IR IR/IGFR	ricone

FIGURE 2N



20E2Bα-3-A10-IR 20E2Bα-3-D3-IR	20E2Bα-4-E2-IR 20E2Bα-4-H1-IR	20E2Bα-3-B4-IR	20E2Bα-4-E1-IR 20E2Bα-4-H8-IR	20E2Bu-4-H12-IR	20E2Bu-3-C8-IR	20E2Bα-3-D11-IR	20Ε2Bα-4-G10-IR	20E2Bu-4-E4-IR	20E2Bu-3-D4-IR	20E2Bu-4-F4-IR	20E2Bu-4-F3-IR	20E2Bα-3-C4-IR	20E2Bu-3-A9-IR	20 <b>E2Bu</b> -3-D1-IR	20E2Bu-3-B6-IR	Clone Design
MVDRDPFYQGLRDLIGRQEKG LGRRGGFYRGLQDLIGTQWPR	HEAGWTFYDAIQCLVGGWCSK CQQWRSFYHAVSCLLGPDDPD	DFDSSPFYRGLRQLLESRSFP	VNLRDPFYQWIEALMDSAGGE LTSSTSFYDALFCLAGLQLCG	CVDRRTFYEGLQCLLGGATGD	PLACADFYQCLSDLIRGGPAW	CSQLVSFYLGMDCLLGRGGTQ	VAQCTDFYACIRSLVRSGSPG	PDIADPFYAFFQGLLRADTPI	PVVLDDFYVALCQLMVQGDCF	VSGRGGFYDAIRDLIGPRDQG	RGRDNQFYHGLWALLLGSGLE	QVFCDNFYHCIETLLGVGQTP	FSGCDNFYSCIQSLWLGPGGV	<u> </u>	SGPMVGFYRGLFSLLSPEDLQ	Sequence xxxxxxFYxxhxxhhxxxxxx

41.9	32.8	40.8	38.8	39.9	37.6	39.2	32.3	38.7	39.2	34.0	32.9	40.6	42.1	37.2	37.5	39.6	37.3	41.6	39.7	:	Ratios ov E-Tag
29.5	Ν	33.6	36.3	34.9	34.8	40.2	30.4	37.6	33.0	32.5	31.3	38.4	38.0	36.9	36.6	36.3	35.1	35.1	34.9	1	over Background IGFsR II
5.6	18.5	20.2	23.5	25.9	27.0	32.3	25.8	32.3	28.2	27.9	27.1	35.5	34.5	33.7	33.6	33.4	32.4	31.7	31.5	;	IR
5.3	1.8	1.7	1.5	1.3	1.3	1.2	1.2	1.2	1.2	1.2	1.2	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	;	Comparisons IGFR/IR IR/I
0.2	0.6	0.6	0.6	0.7	0.8	0.8	0.8	0.9	0.9	0.9	0.9	0.9	0.9	Q.9	. 0.9	0.9	0.9	0.9	0.9	1	risons 11VIGFR



20E2Bβ-4-G7-IR	20E2Bβ-4-H8-IR	20E2Bβ-3-C7-IR	20E2B }-3-C9-IR	20E2B()-3-E5-IR	20E2Bβ-3-D11-IR	20E2B }-4-F6-IR	20E2B }-4-F3-IR	20E2B  -3-E12-IR	20E2B }-4-F7-IR	Cione Design	Cinn
<u>LQPCSGFYECIERLIGVKLSG</u>	LPRQDGFYDALRRLISEGAGG	<b>QSGSGDFYDWLSRLIRGNGDG</b>	FCGGLSFYGCLQELLTWESPT	VHPSAGFYKGLLALIGDSQLG	GSVACDFYCHMWSLVEQPAGT	SEREDPFYRWIQAMVEGVSEG	GDRVPGFYDWIRQLMVDPLEV	GNSGGSFYRYFQLLLDSDGMS	DALNLRFYSYFQHLMEDQVTD	xxxxxx <u>F</u> xx <u>h</u> xxh <u>h</u> xxxxxx	

19.9	25.8	1.5	29.7	24.3	14.8	25.7	25.2	17.2	26.8	:	E-Tag	Ratios ov
25.2	26.9	3.1	24.3	6.9	3.6	3.8	2.0	1.4	3.0	;	IGFSR	Ratios over Background
1.6	13.2	1.5	15.0	4:3	4.2	11.0	7.7	5.5	24.2	;	R	pund
15.8	2.0	2.0	1.6	1.6	0.9	0.4	0.3	0.3	0.1	;	IÇFIVIR	Compa
0.1	0.5	0.5	0.6	0.6	1.2	2.9	3.9	4.0	8.0	:	IR/IGFR	risons



E2B-4-G11-IG E2B-3-D6-IGF E2B-2-B7-IGF E2B-3-C4-IGF	B-4-F9-I B-3-D11- B-3-C11- B-2-B3-I B-2-B3-E12- B-3-E12- B-2-B8-I	0E2B-1-A11 0E2B-3-D4- 0E2B-2-B11 0E2B-2-B11 0E2B-3-C8- 0E2B-2-B2- 0E2B-4-F10	Clone Design 20E2B-1-A6-IGFR 20E2B-3-C6-IGFR 20E2B-4-H3-IGFR 20E2B-3-C2-IGFR 20E2B-3-E3-IGFR 20E2B-3-B-IGFR 20E2B-3-D2-IGFR 20E2B-3-D8-IGFR 20E2B-3-D8-IGFR 20E2B-3-E8-IGFR 20E2B-3-E8-IGFR
RQGTGSFYLMLEQLLVGARGP DSVGDNFYQLLESLVGGHGVG LSSDGQFYRALNLLLQGSAGR ASSASGFYELLQRLAGLGLEV	QPDHSYFYSLLQELVGSEERL LGVTDGFYAALGYLIHGVGQF CMMQDGFYAGLGCLLTAGEGR ICTGQGFYQVLCGLLRGTSAR QGNVLDFYGWIGRLLAKQGSD VATSQGFYSGLSELLQGGGNV	RFSTDGFYQYLLALVGGGPVG NSRDGGFYLQLERLLGFPVTG VVTPVNFYRALEALVRGQRLG QPAPDGFYSALMKLIGRGGVS PGTDLGFYQALRCVVIQGACD AQPCGGFYGLLEQLVGRSVCD	Sequence  XXXXXXFYXXhXXhhXXXXXX  GVRAMSFYDALVSVLGLGPSG VEGRGLFYDLLRQLLARRQNG KLHNLMFYYGLQRLVWGAGLG GNGDGMFYQLLSLLVGRDMHV PDLHKGFYAQLAQLIRGQLLS YSCGDGFYSLLSDLLGGQFRC IQQELTFYDLLHRLVRSELGS GGTEVDFYRALERLVRGQLGL LRIANLFYQRLWDLAFGGGG PVGVQGFYEGLSRLVLGRGGW

23.4	8	20.7	8.9	17.4	13.9	10.3	9.1	•	•		19.0				8.1	15.0	12.3	15.7	20.4	20.7	6.5	22.4	13.1	11.2	17.9	18.6	:	E-Tag	Ratios
•	6.1	17.8	4.5	5.7	6.0	6.2	5.3	15.4	12.2	14.7	17.3	4.9	15.6	10.6	7.9	9.5	7.3	16.7	17.7	12.4	9.7	.16.3	8.9	14.8	16.8	18.1	1 1	IGFR	over Background
ພ ພ	0.9	2.6	0.6	0.8	0.8	0.9	0.7	2.1	1.6	1.9	2.2	0.6	1.8	1.1	0.8	1.0	0.8	1.5	1.6	1.1	0.8	1.3	0.6	1.1	1.1	1.1	:	₹	round
6.2	6.7	6.9	7.0	7.2	7.3	7.3	7.4	7.5	7.6	7.7	7.8	8.1	8.9	9.4	9.6	9.7	9.7	11.1	11.3	11.7	12.8	13.1	13.8	13.9	14.8	16.8	;	IGFIVIR IIVIGFR	Comparison
0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	Q.1	0.1	0.1	0.1	0.1	0.1	:	R/IGFR	S



20E2B-3-C5-IGFR	20E2B-2-B4-IGFR	20E2B-3-E2-IGFR	20E2B-3-E4-IGFR	20E2B-4-G3-IGFR	20E2B-4-G12-IGFR	20E2B-3-C12-IGFR	20E2B-3-E7-IGFR	20E2B-4-H10-IGFR	20E2B-4-G8-IGFR	20E2B-3-E11-IGFR	20E2B-3-E6-IGFR	20E2B-3-C9-IGFR	20E2B-4-H11-IGFR	20E2B-1-A8-IGFR	20E2B-4-H9-IGFR	20E2B-3-E9-IGFR	20E2B-4-H8-IGFR	20E2B-3-D3-IGFR	Design	Clone
RMPSGSFYQGIYELVTRQGGF	ERAGDLFYQWFERLVAGHGLE	VESDVSFYEGLMRLVWWGQGG	GGSQQSFYDVMCMLLQLDPTC	CQQKGDFYAGLVCLLRERASQ	LDSRRGFYDWIKALIGDRDVQ	QHSCRTFYDCIRVLMDDGQLG	<u>Q</u> NGCKDFYCLIDNLIRYGPGG	EASCRTFYCGLMALIGGDDQR	GRALDPFYDQLRDLVARSGGG	SRANNLFYMGLSQLLRDNRGL	RQQASGFYRALHDLMLRTQDY	ROGGSFYELLCGLVGGEVCV	STHSRAFYDAIAQLVGSVLGP	TLRSPTFYDWLEMVLTHGQGG	RCQGTGFYTCIQELIGFGDPD	<b>QAAPQDFYQGLWLLIHRDPTM</b>	PAGPCGFYCGLGLLLHGDQSP	CGSRRDFYGGIICLLGQKGVV	XXXXXXIIXXIIXXXXXXXX	Sequence

6.3	5.8	18.6	24.9	27.2	9.6	6.2	14.4	2.2	11.1	16.5	24.5	17.9	10.7	16.1	4.5	14.7	7.2	21.0	:	Ratios ç E-Tag
2.0	2.3	20.2	22.3	23.8	10.0	6.4	8.8	2.5	14.9	7.7	21.6	19.7	11.0	4.4	5.2	16.2	5.3	16.1	!	ver Backgi IGFR
0.9	1.0	8.7	8.9	9.1	3.8	2.2	3.0	0.8	3.7	1.9	4.7	4.2	2.3	0.9	0.9	2.8	0.9	2.6	1	round IR
2.2	2.2	2.3	2.5	2.6	2.6	2.9	3.0	3.1	4.1	4.1	4.6	4.6	4.8	5.0	5.6	5.8	5.9	6.2	:	Comparison IGFR/IR
																0.2		0.2	:	IR/IGFR



NNRPα-4-D3-IR	NNRPα-4-C7-IR	NNRPq-4-C4-IR	NNRPα-1-B5-IR	NNRPα-4-E7-IR	NNRPβ-4-H12-IR	NNRPβ-4-F2-IR	NNRPα-4-D9-IR	NNRPα-1-B4-IR	NNRPa-1-82-IR	NNRPβ-4-F4-IR	NNRPα-4-D1-IR	NNRPα-4-C3-IR	NNRPα-3-G1-IR	NNRPα-2-C10-IR	NNRPα-1-A1-IR	ŅNRPα-2-D1-IR	$NNRP\beta-4-F7-IR$	NNRPa-3-H6-IR	NNRPq-4-E1-IR	NNRPa-2-C1-IR	$NNRP\beta-4-F3-IR$	NNRP()-4-G6-IR	Design	Clone
TDSQFYSYFESLLETFG	IGVNFYRYFEKLLLDEF	AQDAFYSYFSVLLGEHL	ELGDFYRYF <u>Q</u> LLLADWH	RGNRFYEYFEYLLRDYG	RDGAFYRYFEDLLIAVD	KHEQFYEYFRNLLGAMS	<b>DPGAFYRYFAQLMDTWN</b>	LSSGFYRYFTGLLSDG $Q$	GGEAFYRYFWGLLTEWE	GHAEFYGYFQGLLDSYL	GRESFYGYFLDLLQETV	WGGEFYRYFVQLLSSED	WRDPFYRYFQDLLEGER	RGGAFYRYFEGLLSQHN	PTGPFDRYFARRLVWRG	GGGQFYRYFIDMLVLDI	RREGFYHYFQSLLDEYG	WGRSFYRYFETLLAQGI	LDRQFYRYFQDLLVGFM	EGWDFYSYFSGLLASVT	HYNAFYEYFQVLLAETW	RWPNFYGYFESLLTHFS	XXXXXXFYRYFXXLLXXXXXX	Sequence

16.4	4.5	17.6	14.1	9.4	5.2	21.6	7.6	19.1	14.8	19.5	16.2	17.9	18.9	18.8	15.2	18.4	0.7	19.1	11.5	19.7	8.6	10.1		Ratios o E-Tag
13.5	11.2	17.6	5.4	21.9	13.8	20.9	16.9	6.3	· 8 · 4	16.0	12.7	12.9	4.2	3.8	1.3	1.5	0.9	2.1	6.5	2.0	1.3	1.9	;	s over Background g IGFR IR
17.9	14.9	22.3	7.1	29.7	20.0	30.8	25.7	9.2	12.9	25.6	23.2	25.7	8.6	8.8	3.1	3.7	2.3	6.0	21.2	10.9	13.6	20.1		
0.8	0.8	0.8	0.8	0.7	0.7	0.7	0.7	0.7	0.7	0.6	0.5	0.5	0.5	0.4	0.4	0.4	0.4	0.3	0.3	0.2	0.1	0.1	!	Comparison IGFR/IR
1.3	1.3	1.3	1.3	1.4	1.5	1.5	1.5	1.5	1.5	1.6	1.8	2.0	2.1	2.3	2.4	2.5	2.7	2.9	3.2	5.3		10.6		ons IR/IGFR



NNRPy-4-A8-IR	NNRPγ-4-A6-IR	NNRP()-4-H10-IR	NNRPβ-4-H9-IR	NNRP 3-4-H3-IR	$NNRP\{\}-4-G8-IR$	NNRPβ-4-F10-IR	$NNRP\beta-4-F8-IR$	NNRPG-4-E10-IR	$NNRP\alpha - 4 - E8 - IR$	NNRPa-4-E5-IR	NNRPα-4-D10-IR	$NNRP\alpha - 4 - D8 - IR$	NNRPa-4-C11-IR	$NNRP\alpha - 1 - A7 - IR$	NNRPγ-4-A3-IR	$NNRP\beta-4-F12-IR$	NNRP 3-4-F9-IR	$NNRP\beta - 4 - F1 - IR$	NNRPa-4-D11-IR	NNRPα-4-D7-IR	NNRPu-4-C12-IR	NNRPα-4-C6-IR	NNRPu-4-C5-IR	NNRPα-4-C1-IR	NNRP/3-4-H2-IR	NNRP }-4-G10-IR	Design	Clone
MDAGFYGYFSDLLANWG	EEEGFYGYFYRLLGVER	WHSDFYRYFLSLLQEDG	DGGAFYRYFEALLGELD	FGGAFYRYFEALLGEMG	GDRGFYRYFEWLLNDFG	ETGGFYGYFQALLATYH	SDEGFYRYFAQLLYGVT	VHGEFYRYFESLLRETF	SSGGFYRYFSQLLTEMN	TSNWFYQYFTDLLAGED	EYSGFYGYFNHLLGSLG	<b>PHRGFYRYFLYQLAGNV</b>	LGGYFYRYFEDLLNIIQS	STVSFYRYFYALLQSPC	GSLDFYSYFWERLGLGP	MGSSFYRYFETLLGQGL	FHRGFYRYFINLLSGDA	RHINFYGYFDDLLATWH	?GLNFYRYFVGLLTDTL	DPNAFYRYFEGLLWREH	FAGSFYRYFEQLLLSEQ	GQNGFYRYFDTLLADWV	GRGGFYQYFLDLLQTEA	SGSWFYRYFEELLLQSG	TGRGFYRYFEGLLEDWM	SSREFYSYFSGLLTTAL	XXXXXXFYRYFXXLLXXXXXX	Sequence

Ratios o	Ratios over Background	puno	Comparisons	ons
E-Tag	IGFR		IGFIVIR	IK/IGFR
8.8	8.7	11.7	0.7	<b>1</b> .3
4.9	19.9	25.3	0.8	1.3
15.5	18.0	21:1	0.9	1.2
18.0	23.3	26.9	0.9	1.2
	13.6	15.7	0.9	1.2
12.3	16.7	19.9	0.8	. 1.2
10.2	23.7	27.9	0.8	1.2
5.4	19.3	22.3	0.9	1.2
21.7	23.0	28.6	0.8	1.2
.10.1	18.4	22.5	0.8	1.2
4.5	13.5	16.6	0.8	1.2
16.4	22.3	26.8	0.8	1.2
	1.2	•	0.9	1.1
	19.7	21.2	0.9	1.1
	17.6	20.1	0.9	1.1
6.4	17.2		0.9	1.1
13.2	26.1	27.6	0.9	1.1
8.7	22.9	24.2	0.9	1.1
	N	13.2	0.9	1.1
	22.9		0.9	1.1
5.3	17.9	19.1	0.9	1.1
	27.2	28.9	0.9	1.1
3.9	24.2	25.7	0.9	1.1
4.1	6	29.3	0.9	1.1
3.4	22.3	24.6	0.9	1.1
14.9	S	27.6	0.9	1.1
9.8	N	24.7		1.1

FIGURE 2P (Con't)

OIP	EVCZ
O HUL	" JOBS 335
PIETS.	RAUCHARIT

Clone	Seamence	E-Tao	GFR	≅	ICER/IR IR/	₹
Design	XXXXXFYRYFXXLLXXXXXX		:	: (	:	4
NNRPy-4-A10-IR	SGFAFYQYFQELLAGHD	7.6	20.3	22.0	0.9	
NNRPγ-4-B6-IR	GDGGFYGYFASLLSGEG	12.2	22.3	24.2	0.9	
NNRPy-4-B9-IR	<b>EANGFYRYFYDLLQDFG</b>	6.7	22.9	25.9	0.9	
NNRPα-4-C8-IR	AVNGFYRYFNRLLESVE	8.5	16.3	16.0	1.0	
$NNRP\alpha - 4 - C9 - IR$	QQDGFYRYFLDLLDEVA	5.6	20.7	19.9	1.0	
NNRPu-4-C10-IR	ISQGFYGYFSRLLQDTE	6.7	16.5	17.2	1.0	
$NNRP\alpha - 4 - E11 - IR$	YSTGFYRYFLDLLDGMP	6.0	20.3	20.9	1.0	
NNRP 3-4-F11-IR	PNGDFYRYFLDLLGSVG	7.7	21.8	21.9	1.0	
$NNRP\beta-4-G2-IR$	RHQAFYSYFRDLPRECP	19.1	24.7	25.6	1.0	
$NNRP\beta-4-G9-IR$	ETEGFYRYFEELLAQVA	7.8	27.3	26.4	1.0	
$NNRP\beta-4-H7-IR$	AGDRFYDYFDRLLADYD	2.6	26.6	27.9	1.0	
NNRP() - 4 - H8 - IR	GGSGFYRYFWGLLAE <u>Q</u> E	3.6	23.0	24.1	1.0	
NNRPγ-4-B1-IR	LLNRLYRYFAGAEGWFG	17.6	24.5	23.4	1.0	
NNRPγ-4-B10-IR	DGSGFYRYFEMLLGSGL	5.5	18.3	19.0	1.0	
NNRPα-1-B3-IR	RDMAFYRYFSHLLESFQ	16.4	13.4	12.7	1.1	
$NNRP\alpha - 2 - C2 - IR$	GNAGFYRISRILWOGTE	22.5	24.4	21.3	1.1	
$NNRP\alpha - 2 - C3 - IR$	GNAGFYRYFADLMAGYE	19.6	21.7	19.7	1.1	
$NNRP\alpha - 2 - D10 - IR$	YQAAFYRYFATLLSTTD	17.8	6.3	5.4	1.2	
$NNRP\alpha - 3 - E11 - IR$	GGLGFYRYFQLLLGSSG	12.9	10.8	9.6	1.1	
$NNRP\alpha - 3 - F5 - IR$	DGSGFYGYFDFVLRQFE	25.1	18.3	17.0	1.1	
NNRPα-3-F8-IR	VGSGFYRYFDQLLGMYG	22.2	15.7	13.9	1.1	
NNRPα-3-F10-IR	YGTDFYLYFDQLLLQYG	20.5	14.6	13.1	1.1	
$NNRP\alpha - 3 - G7 - IR$	FNSSFYLYFRDLLNTVG	21.0	18.3	15.6	1.2	
$NNRP\alpha - 4 - C2 - IR$	RAAGFYRYFEDLLGARG	25.5	25.1	23.3	1.1	
NNRPα-4-D12-IR	TGAGFYRYFIDLLGETG	14.7	19.7	18.5	1.1	
NNRPβ-4-G3-IR	RDLEFYGYFQELLRLNF	14.6	27.8	25.7	1.1	
NNRP 3-4-G4-IR	GMGPFYRYFIDLLRESD	20.0	28.6	24.9	1.1	
NNRPy-4-A5-IR	HGDGFYQYFMEVLRL <u>Q</u> N	17.0	29.0	27.3	1.1	

FIGURE 2P (Con't)



ŅNRPβ-4-H6-IR	NNRP()-4-G11-IR	NNRPa-4-E12-IR	NNR Pα - 3 - H4 - IR	NNRPφ-3-G4-IR	NNRPa-3-F4-IR	NNRPα-3-E4-IR	NNRPα-3-E2-IR	NNRPα-2-D11-IR	NNRPα-2-D5-IR	NNRPα-2-D2-IR	NNRPα-2-C9-IR	NNRPa-2-C5-IR	NNRPα-1-B8-IR	NNRPy-4-B2-IR	NNRPα-3-G12-IR	ŅNRPα-3-G11-IR	NNRPa-3-G10-IR	NNRPa-3-G8-IR	NNRPα-3-G2-IR	NNRPq-2-D12-IR	NNRPα-2-C12-IR	NNRPα-2-C11-IR	NNRPq2-C7-IR	NNRPa-1-87-IR	NNRPα-1-A5-IR	NNRPy-4-B8-IR	NNRPγ-4-A12-IR	<b>Design</b>	Clone
KYSGFYEYFNALLGRRE	SSRGFYRYFRELLADSW	AGRGFYRYFEHLLAGRE	DGGAFYRYFMDLLGAHE	HPRDFYRYFERLLNQVD	WDTGFYRYFIELLEDRD	QNGSFYRYFIALLGDSG	<b>ADGGFYGYFAALLGSVS</b>	SQSSFYRYFESLLEDNP	LNSGFYGYFVQLLSGHQ	LGGAFYRYFAQLLNSHV	SKSAFYRYFDELLGNSG	QALSFYRYFERLLDEVS	GRMTRLIVRSTVISRELLHYSL	RHKAFYRYFEELLOKNV	EGSGFYRYFEKLLLQSP	RQQDFYRYFRQLLLEEV	QNDAFYSYFNSLLQAYT	GVSGFYRYFQSLLDSYG	TRGGFYRYFEDLLQVYS	RSTLFYRYFQNLLEEVG	LSDGFYRYFEQLMGARS	NSAAFYRYFEQLLEREV	GDRGFYRYFEGLLASVG	GSSGFYRYFNMLMLSQT	ĻSTSFYQYLAGĻĻRGDR	<b>PARGEYRYFESLLLGSS</b>	AFYRYFRDLLFSGF	XXXXXXFYRYFXXLLXXXXXX	Şequence
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										•																			
					*										,		,		•			٠							
2.2	6.6	4.3	17.7	20.9	24.9	23.0	24.4	12.3	21.7	26.1	22.9	18.1	16.1	22.8	11.7	12.0	18.8	14.7	20.8	11.5	14.3	20.1	19.6	19.2	2.3	6.1	4:9		E-Tag
16.1	18.4	15.4	17.6	20.4	25.1	22.3	25.5	10.8	21.1		21.7	19.2	10.1	30.3	11.8	10.3	16.5	11.0	20.7	11.4	10.1	20.0	20.0	15.7	1.4	21.3	16.3		IGFR
11.7	13.1	10.8	11.6	14.1	17.6	14.7	18.3	7.8	•			•		25.3				•						12.4	1.1	19.9	14.9	;	₹
1.4	1.4	1.4	1.5	1.5	1.4	1.5	1.4	1.4	1.4	1.5	1.3	1.4	1.5	1.2	1.3	1.2	1.2	1.2	1.3	1.2	1.2	1.2	1.2	1.3	1.2	1.1	1.1	1	ICFIVIR IR/IC
0	0	0	0	0	0	0	0	•		0		0	0	0	0	0	0	<b>O</b> .	0	0	0	0	0	0	0	0	0		IR/IGI

FIGURE 2P (Con't)



LKDGFYDYFWQRLHLGS	NNRPy-4-B11-IR
EGSGFYGYFFSLLGLQG	NNRPy-4-A9-IR
RFDPFYSYFVNLLGASA	NNRPy-4-A7-IR
IIGGFYSYFNSVLRLGT	NNRPy-4-A1-IR
NSAAFYGYFSQLLAQIR	$NNRP\alpha-2-C6-IR$
DVGDFYRYFGLLLTSDR	NNRPα-1-B6-IR
MHGSFYRYFQDLLQAPP	$NNRP\alpha - 3 - H2 - IR$
VGDAFYRYFQGLLRQDQ	$NNRP\alpha-3-F6-IR$
$ extsf{NYSQFYRYFEMLLEGDV}$	$NNRP\alpha-2-D6-IR$
CEDAFYRYFVNLLGQGC	$NNRP\alpha-1-A9-IR$
GDRAFYRYF <u>Q</u> RQLEGWG	NNRPa-1-A8-IR
LGGGFYRYFNLLVMGSG	$NNRP\alpha-3-H9-IR$
QIDEFYRYFADQLRGFA	NNRPα-3-G6-IR
QHRLFYSYFAELLGRDT	NNRPa-3-F9-IR
RNSGFYRYFQHLVSEWE	$NNRP\alpha - 3 - E6 - IR$
AAGFYGYFYSLLGDQT	$NNRP\alpha - 1 - A3 - IR$
WRGAFYRYFQTLLSDEG	$NNRP\alpha - 3 - H5 - IR$
<u>Q</u> GGGFYHYFLSLLEEVG	$NNRP\alpha-3-H3-IR$
RSGLFYRYFEELLQGAI	$NNRP\alpha-3-E5-IR$
SQGGFYRYFEKLLDEVT	$NNRP\alpha - 3 - E1 - IR$
GGSSFYRYFEQLLAQWE	NNRPa-2-D8-IR
DTNAFYRYFEGLLWSEH	NNRPQ-2-D7-IR
FOSSFYGYFESLLMSYK	$NNRP\alpha-1-B1-IR$
DYTAFYGYFNNLLRTSG	$NNRP\beta - 4 - H11 - IR$
XXXXXXFYRYFXXLLXXXXXX	Design
Sequence	Clone

E-Tag IGFR IR IGFR/IR IR/IGFR	12.4	18.7 11.5 1.6	21.8 13.2 1.6	19.8 12.2 1.6	20.5 12.9 1.6	24.5 15.5 1.6	19.1 12.2 1.6	18.0 11.1 1.6	14.9 7.9 1.9	19.0 9.6 2.0	18.8 9.6 1.9	17.7 9.0 2.0	13.1 6.9 1.9	13.8 5.7 2.4	15.2 5.6 2.7	18.5 6.8 2.7	19.5 7.9 2.5	18.9 8.5 2.2	11.5 3.9 3.0	19.2 4.1 4.7		10.9 1.8 6.0	10.9 1.8 6.0 6.3 1.3 4.9
/IGFR	0.7	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.5	0.5	0.5	0.5	0.5	0.4	0.4	0.4	0.4		0.4	0.4	0.4	0.3	0.4
2.3     12.4     9.0     1.4     0.7       18.8     18.7     11.5     1.6     0.6       21.0     21.8     13.2     1.6     0.6       20.2     19.8     12.2     1.6     0.6       20.0     20.5     12.9     1.6     0.6       20.0     24.5     15.5     1.6     0.6       19.8     19.1     12.2     1.6     0.6       19.9     18.0     11.1     1.6     0.6       24.4     14.9     7.9     1.9     0.5       23.1     19.0     9.6     2.0     0.5       22.4     17.7     9.0     2.0     0.5       18.3     13.1     6.9     1.9     0.5       18.3     13.1     6.9     1.9     0.5       18.3     13.1     6.9     1.9     0.5       18.3     13.1     6.8     2.7     0.4       19.4     18.5     6.8     2.7     0.4       19.9     18.9     8.5     2.2     0.4       19.9     18.9     8.5     2.2     0.4       14.1     11.5     3.9     3.0     0.3       18.4     19.2     4.1     4.7     0.2 <td>18.7       11.5       1.6         21.8       13.2       1.6         19.8       12.2       1.6         20.5       12.9       1.6         24.5       15.5       1.6         19.1       12.2       1.6         14.9       7.9       1.9         19.0       9.6       2.0         11.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.0       1.4       7.1</td> <td>21.8       13.2       1.6         19.8       12.2       1.6         20.5       12.9       1.6         24.5       15.5       1.6         19.1       12.2       1.6         18.0       11.1       1.6         14.9       7.9       1.9         19.0       9.6       2.0         117.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.0       1.4       7.1</td> <td>19.8       12.2       1.6         20.5       12.9       1.6         24.5       15.5       1.6         19.1       12.2       1.6         14.9       7.9       1.9         19.0       9.6       2.0         18.8       9.6       1.9         17.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.0       1.4       7.1</td> <td>20.5       12.9       1.6         24.5       15.5       1.6         19.1       12.2       1.6         14.9       7.9       1.9         19.0       9.6       2.0         18.8       9.6       1.9         17.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1</td> <td>24.5     15.5     1.6       19.1     12.2     1.6       18.0     11.1     1.6       14.9     7.9     1.9       19.0     9.6     2.0       18.8     9.6     1.9       17.7     9.0     2.0       13.1     6.9     1.9       13.8     5.7     2.4       15.2     5.6     2.7       19.5     7.9     2.5       18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1</td> <td>19.1     12.2     1.6       18.0     11.1     1.6       14.9     7.9     1.9       19.0     9.6     2.0       18.8     9.6     1.9       17.7     9.0     2.0       13.1     6.9     1.9       13.8     5.7     2.4       15.2     5.6     2.7       18.5     6.8     2.7       19.5     7.9     2.5       11.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1</td> <td>18.0       11.1       1.6         14.9       7.9       1.9         19.0       9.6       2.0         18.8       9.6       1.9         17.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         19.5       7.9       2.5         118.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1</td> <td>14.9     7.9     1.9       19.0     9.6     2.0       18.8     9.6     1.9       17.7     9.0     2.0       13.1     6.9     1.9       13.8     5.7     2.4       15.2     5.6     2.7       18.5     6.8     2.7       19.5     7.9     2.5       18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1</td> <td>19.0       9.6       2.0         18.8       9.6       1.9         17.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1</td> <td>18.8       9.6       1.9         17.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1</td> <td>17.7     9.0     2.0       13.1     6.9     1.9       13.8     5.7     2.4       15.2     5.6     2.7       18.5     6.8     2.7       19.5     7.9     2.5       18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1</td> <td>13.1     6.9     1.9       13.8     5.7     2.4       15.2     5.6     2.7       18.5     6.8     2.7       19.5     7.9     2.5       18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1</td> <td>13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1</td> <td>15.2       5.6       2.7         18.5       6.8       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1</td> <td>18.5       6.8       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1</td> <td>19.5     7.9     2.5       18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1</td> <td>18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1</td> <td>11.5 3.9 3.0 19.2 4.1 4.7 10.9 1.8 6.0 6.3 1.3 4.9 10.0 1.4 7.1</td> <td>19.2 4.1 4.7 10.9 1.8 6.0 6.3 1.3 4.9 10.0 1.4 7.1</td> <td>10.9 1.8 6.0 6.3 1.3 4.9 10.0 1.4 7.1</td> <td>6.3 1.3 4.9 10.0 1.4 7.1</td> <td>10.0 1.4 7.1</td> <td></td>	18.7       11.5       1.6         21.8       13.2       1.6         19.8       12.2       1.6         20.5       12.9       1.6         24.5       15.5       1.6         19.1       12.2       1.6         14.9       7.9       1.9         19.0       9.6       2.0         11.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.0       1.4       7.1	21.8       13.2       1.6         19.8       12.2       1.6         20.5       12.9       1.6         24.5       15.5       1.6         19.1       12.2       1.6         18.0       11.1       1.6         14.9       7.9       1.9         19.0       9.6       2.0         117.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.0       1.4       7.1	19.8       12.2       1.6         20.5       12.9       1.6         24.5       15.5       1.6         19.1       12.2       1.6         14.9       7.9       1.9         19.0       9.6       2.0         18.8       9.6       1.9         17.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.0       1.4       7.1	20.5       12.9       1.6         24.5       15.5       1.6         19.1       12.2       1.6         14.9       7.9       1.9         19.0       9.6       2.0         18.8       9.6       1.9         17.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1	24.5     15.5     1.6       19.1     12.2     1.6       18.0     11.1     1.6       14.9     7.9     1.9       19.0     9.6     2.0       18.8     9.6     1.9       17.7     9.0     2.0       13.1     6.9     1.9       13.8     5.7     2.4       15.2     5.6     2.7       19.5     7.9     2.5       18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1	19.1     12.2     1.6       18.0     11.1     1.6       14.9     7.9     1.9       19.0     9.6     2.0       18.8     9.6     1.9       17.7     9.0     2.0       13.1     6.9     1.9       13.8     5.7     2.4       15.2     5.6     2.7       18.5     6.8     2.7       19.5     7.9     2.5       11.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1	18.0       11.1       1.6         14.9       7.9       1.9         19.0       9.6       2.0         18.8       9.6       1.9         17.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         19.5       7.9       2.5         118.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1	14.9     7.9     1.9       19.0     9.6     2.0       18.8     9.6     1.9       17.7     9.0     2.0       13.1     6.9     1.9       13.8     5.7     2.4       15.2     5.6     2.7       18.5     6.8     2.7       19.5     7.9     2.5       18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1	19.0       9.6       2.0         18.8       9.6       1.9         17.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1	18.8       9.6       1.9         17.7       9.0       2.0         13.1       6.9       1.9         13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1	17.7     9.0     2.0       13.1     6.9     1.9       13.8     5.7     2.4       15.2     5.6     2.7       18.5     6.8     2.7       19.5     7.9     2.5       18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1	13.1     6.9     1.9       13.8     5.7     2.4       15.2     5.6     2.7       18.5     6.8     2.7       19.5     7.9     2.5       18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1	13.8       5.7       2.4         15.2       5.6       2.7         18.5       6.8       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1	15.2       5.6       2.7         18.5       6.8       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1	18.5       6.8       2.7         19.5       7.9       2.5         18.9       8.5       2.2         11.5       3.9       3.0         19.2       4.1       4.7         10.9       1.8       6.0         6.3       1.3       4.9         10.0       1.4       7.1	19.5     7.9     2.5       18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1	18.9     8.5     2.2       11.5     3.9     3.0       19.2     4.1     4.7       10.9     1.8     6.0       6.3     1.3     4.9       10.0     1.4     7.1	11.5 3.9 3.0 19.2 4.1 4.7 10.9 1.8 6.0 6.3 1.3 4.9 10.0 1.4 7.1	19.2 4.1 4.7 10.9 1.8 6.0 6.3 1.3 4.9 10.0 1.4 7.1	10.9 1.8 6.0 6.3 1.3 4.9 10.0 1.4 7.1	6.3 1.3 4.9 10.0 1.4 7.1	10.0 1.4 7.1	



Clone	Sequence
)esign	XXXXXXXXXXXXXXXXXX
₹20-4-F9-IGFR	PLAELWAYFEHSEQGRSSAH
R20-4-H4-IGFR	PVLSGLĻRYFAGGPLG <u>Q</u> PQS
₹20-4-F9-IGFR	GGYLDDLWHYFRDGQALQPW
₹20-4-D6-IGFR	VDQRQGGWLLALENYFRSTV
₹20 - 4 -G2 - IGFR	DVPAGGLLRQMWVYFRDSDP

Ratios ov	er Backgro	ψnφ	Comparisons	risons	
Ę-Tag	E-Tag IGFsR IF	R	IGFR/IR	IR/IGFR	
:	1	:	:	:	
33.1	19.3	1.0	19.3	0.1	
24.1	5.6	3.2	1.8	0.6	
2.5	2.4	1.4	1.7	0.6	
6.1	2.9	1.9	1.5	0.7	
ر. و	2.2	2.0	1.1	0.9	



Clone
Design
20C-3-F3-IGFR



٠	rB6-4-D7-IR	rB6-4-B8-IR	rB6-4-G8-IR	rB6-4-C11-IR	rB6-4-G12-IR	rB6-4-G12-IR	rB6-3-C6-IR	rB6-4-H12-IR	rB6-4-C7-IR	r86-3-A6-IR	r86-4-B9-IR	rB6-4-E8-IR	rB6-4-A8-IR	rB6-4-D11-IR	rB6-4-F12-IR	rB6-4-E11-IR	rB6-3-E6-IR	rB6-4-A12-IR	r86-4-E7-IR	Design	Clone
	DDVLNYLLGYFRQSDGL	DNWLSALMAYFMGSGES	<b>DGLLWQLWDYFALSEHR</b>	MDPLRGLLMYFSQGGLV	<b>PPTLFGLLRYFQESGIA</b>	DPWLAWLGRYFGETATG	DDMLRQLWLYFEASAGG	ARPLDWLLDYFKQGARG	DGVLEGLLSYFTSTNSH	GDQLAWLLAYFQSDGSD	GDILDALLRYFEFGVDT	DDALEWLLNYFQNGHVQ	DSILRELRDYFAPYSHC	PMNLSELWDYFRLKPGR	DGVLEELFSYFSATVGP	DOELGWLRGYFEWTARD	ADELEWLLDYFMHQPRP	<b>LDALDRLMRYFEERPSL</b>	LDPLDALLQYFWSVPGH	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	Sequence

24.1	31.1	37.3	26.6	33.3	37.7	34.2	26.0	-	Ñ	N	ũ	ū	-	Ö	_	9.0	34.9	26.4	:	E-Tag	Ratios ov
29.4	28.6	7.4	18.7	7.6	6.1	19.1	10.0	2.6	2.9	17.2	9.7	2.4	15.7	1.0	1.6	1.0	1.0	1.0	:	<b>IÇFSR</b>	er Backgro
1.0	1.0	1:3	4.7	3.5	3.1	12.8	7.2	2;3	2.8	21.7	15.9	4.6	30.2	3.4	. 5.9	4.8	12.0	15.5	1	īR	ψnφ
						1.5						0.5	0.5	0.3	0.3	0.2	0.1	Q.1	1	ICFR/IR	Compai
						0.7					1.6	. 1.9	1.9		3.7			15.5	:	IR/IGFR	risons



rB6-3-A3-IGFR rB6-4-E9-IGFR	rB6-3-B3-IGFR rB6-4-G7-IGFR	rB6-3-E5-IGFR	rB6-3-H2-IGFR	B6-4-B8-IGF	B6-3-C5-IGF	B6-3-B5-IGFR	186-4-812-IGFR	-4-E8-IGFR	rB6-3-G6-IGFR	rB6-4-F7-IGFR	rB6-4-F12-IGFR	rB6-4-C11-IGFR	rB6-3-D7-IGFR	rB6-3-B2-IGFR	rB6-3-£1-IGFR	rB6-4-F9-IGFR	rB6-3-D6-IGFR	rB6-4-D10-IGFR	rB6-3-D4-IGFR	rB6-3-B6-IGFR	rB6-3-F5-IGFR	rB6-4-B9-IGFR	rB6-3-E6-IGFR	rB6-4-B19-IGFR	Design	Clone
QDVLRSLLSYFMGNGDV DGVLSKLWEYFKIQGND	DKVLRLLGEYFATHSKG QGPLAWLRDYFASGTRS	VDILSELWDYFRRGEEG	<	DEVLGRLWAYFAQESLG	GGVLAALERYFRVSAGD	DVILGGLWDYFASGGGH	DGMLSRIWEYFAGTNVD	PGILLDLWRYFASAPDQ	DELLDRLWQYFQVGGDL	SGILGQLLRYFKGAGGG	NEVLEGLESYFVY?ANG	DSVLQYLLNHFGADSKQ	QDVLGALQRYFASGEPW	DEILGALYSYFSLSGGA	DGVLAALEAYFRHGPRD	DSVLRSLYSYFASGDIA	DPPLGGLWTYFSRSDPG	SGVLADLFRYFQRHPWP	QDLLGRLWLYFAETDTV	DGILGLLMAYFVES?RV	<b>PROLOWINDA EHTLIDIS</b>	DGVLASLWRYFVSGGTL	RWPLSALMDYFRRSDGV	RPVLGWLFDYFVASDPM	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	Sequence

37.3		37.4				•	38.7	17.2	36.3	34.9	37.6	34.0	8	38.1	ũ	-	N	O	34.3		•	31.2	37.4	33.2	39.2	37.6	33.1	:	E-Tag	Ratios over
20.1	4	10.0	•	•	22.4	•		6.1	28.9	14.5		•	7.3		•				28.3	٠	•	20.7	13.3	15.6	26.3	•	26.9	:	IGFsR	er Backgro
4.8	1.0	2.1	1.0	4.0	4.2	4.1	2.9	1.0	4.5	2.2	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	3.0	1.0	1.0	2.0	1.0	1.0	1.0	1.0	1.0	;	IR	und
4.2	4.7	4.8	4.8	5.1	5.3	5.4	5.4	6.1		•	6.9	7.1	7.3	7.3	7.6	7.6	8.8	9.3	9.4	9.9	10.1	10.4	13.3	15.6	26.3	26.6	26.9	:	ICFR/IR	Compa
0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1		0.1		0.1	0.1	0.1	0.1	<0.1	<0.1	<0.1	:	IR/IÇFR	risons



rB6-3-C4-IGFR	rB6-4-G12-IGFR	rB6-4-H12-IGFR	rB6-3-G3-IGFR	rB6-4-E11-IGFR	rB6-4-B11-IGFR	rB6-4-D11-IGFR	rB6-4-C9-IGFR	rB6-3-G5-IGFR	rB6-4-G8-IGFR	rB6-3-C2-IGFR	rB6-3-E2-IGFR	rB6-4-H8-IGFR	rB6-4-A8-IGFR	rB6-4-D8-IGFR	rB6-3-H5-IGFR	r¤6-3-F6-IGFR	rB6-3-A1-IGFR	rB6-4-C10-IGFR	r86-4-87-IGFR	rB6-3-F1-IGFR	Design	Clone
GGILD?LQDYFRSTDVG	IQSL*DLLQYFVSSPSV	ESPLDALRAYFSGRRNW	DEALLWLMRYFRGSPSP	IKTLNDLLAYFRGDLDV	RDVLDGLREYFRASVGG	FDVLTWLGRYF * MNTGK	DDVLVTLFQYFRASTGV	WRILDRLLAYFKESQGD	DRALGPLWRYFMVNNGQ	SAVLEYLLAYFARTGAA	DNVLEGLWSYFALWSQL	?PPLDALWEYFTGTARD	DGVLGQLWQYFAQYPGS	DSILRELRDYFARTHIA	<b>LALLPMLWDYFVATDPQ</b>	DLILQSLLDYFQGRPVG	DRLLSGLWAYFAGNGGS	GGPLQGLYTYFKQSPVC	?DVLKKL?VYFELSGGA	NTILGDLWRYFAGSGGM	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	Sequence

37.1	36.7	40.1	31.6	38.1	25.2	36.6	7	N	38.7	$\mathbf{H}$	Ó	8	$\vdash$	9	S	S	$\vdash$	2	$\mathbf{H}$	σ	:	Ratios o E-Tag
6.2	32.5	2.8	8.7	29.8	4.2	5.5	30.2	2.0	5.5	2.1	2.2	33.0	30.6	22.5	18.1	J. 5	3.5	3.7	11.4	5.8	1.	ver Backgro IGFsR
	31.4																			1.4	1	lR
0.5	1.0	1.1	1.2	1.3	1.8	1.8	2.0	2.0	2.1	2.1	2.2	2.9	2.9	3.0	3.2	3.5	3.5	3.7	3.9	4.1	:	Compar IGFR/IR I
2.2	1.0	0.9	0.8	0.7	0.6	0.5	0.5	0.5	0.5	0.5	0.5	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.2	!	isons R/IGFR



Clone Design R2Oβ-4-F8-IR 

Ratios over Background E-Tag IGFsR IR

Comparisons IGFR/IR IR/IGFR

15.4



	FO.F	Ó	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	F81	Des	
	5-4-87	4	5-3-B	5-3-A	5-4-F	5-3-B	5-4-G	5-3-A	5-4-G	5-4-G	5-3-C	5-3-B	5-3-C	5-3-D	5-3-A	5-3-B	5-3-A	5-4-H	5-3-A	5-3-D	5-3-A	5-4-H	5-3-C	5-3-P	5-3-Q	5-3-B	5-4-H	ign	116
•	7 - 1 5	. 4	6-IR	2-IR	4 - IR	5 - IR	5-IR	8-IR	6-IR	9-IR	1 - IR	4 - IR	4 - IR	2-IR	4-IR	3 - IR	3 - IR	4 - IR	1-IR	7 - IR	5-IR	3-IR	5 - IR	4 - IR	1 - IR	1-IR	9-IR		
																												•	
(	< <	, Č	HLCV	QLCV	PLCV	HLCV	PLCV	QLCV.	HLCV	SLCA	HLCV	HLCV	QLCV	HLCV	YLCV	KLCV	нісл	PLCV	HLCE	QLCV	PLCV	NLCDL	HLCVV	НГСЛГ	Δηςν	HLCV	PLCV	L L	Seducac
		回	VEELI	LEELVI	HEELF	LEELFI	LEELF	LEELF	1 <u>aŏ</u> aan	LEEQF	LEELFI	LEELFWGGN	LEQLF	<b>LEELLWG</b>	LEELSI	LEELF	٦,	LEELF	LEELFI	LEELFI	LEEQFI	LEVLFWGAS	EELF	LEELFWGAS	<b>LEELF</b>	<b>JEELF</b>	สาสสา	EL	nce
	NGASLE	ASL	WGASLF	WGASLF	ATSÓDM,	WGASLF	WGAALF	WGASLF	WGASLF	FWGĄALF	WGASLY	<b>VGGNLF</b>	<b>HUSESLF</b>	<b>VGASLF</b>	WGASLF	WGASLF	WGASRF	<b>HUSESLF</b>	WGASLF	WGASEF	FWGASLF	NGASLF	WGASLF	<b>JGASLF</b>	FWGASRF	FWGASLF	MŠTPLF	FWGASLF	
		GQCA	۵,	ดั	ດັ	ดั	a	osogo	DGCAG	a	ra <u>o</u> csa	osogs	ດັ	AQCSG	oso <u>ō</u> os	ดั	ດັ	Õ		S.	ດັ	χ	G.	ິດ		AQCVG	x SOOD:	GYCSG	
•	<i>-</i> u.				••	••					•			••						~-	٠,	•	٠.		4,3	•-	•	. 44	



HLCVLEDLFWGASLFDQC HLCDLEVLFWGASLFGQC QLCILEEQFWGTSLFGYC	F815-3-D11-IR F815-4-E7-IR F815-3-A10-IR F815-3-B11-IR
CVLEELFWGASQ CVLEELFWGASL CVLEERFWGVSL CVLEERFWGVSL	15-4-E12-I 15-4-E12-I 15-4-F8-IR 15-3-C7-IR 15-4-F10-I
ELFWGASL ELFWGVSL ELFWGVSL ELFWGGAL	815-3-88-1 815-3-82-1 815-3-82-1 815-3-03-1 815-3-87-1 815-3-87-1
CALEELFWGAAL CVLEELFWGAAL CVLEELFWGAAL CVLEELFWGAAL CVLEELFWGAAL	15-4-F1-IR 15-4-G8-IR 15-4-H12-I 15-4-G3-IR 15-4-G3-IR 15-4-E10-I
tovieelewgast Lovieelewgsst Lovieelewgsst Lovieelewgsst Lovieellwgsst Lovieellwgsst	Joure lesign 815-3-A6-I 815-3-D3-I 815-3-B12- 815-4-G10- 815-4-E3-I 815-4-E3-I

Ratios ov	er Backgro	E D C	Compa	risons
E-Tag	ICFSR	≅	ICFIVIR	HVIGER
	. [	;	•	:
	1.1	39.0	<0.1	36.2
33.8	1.0	•	<0.1	36.2
33.2	1.0	35.7	<0.1	36.2
35.4	1. O	37.2	<0.1	36.1
32.4	1.0	•	<0.1	36.1
33.2	1.0	•	<0.1	•
•	0.9	•	<0.1	36.0
6	1.1	•	<0.1	35.9
30.5	0.9	•	<0.1	35.9
۲.	1.0	•		35.7
2	1.0	36.1		
35.4	1.0	•		
2.	1.0		<0.1	35.3
33.6	1.0	•		5
۲.	1.0			5
30.1	1.0	35.3	<0.1	35.3
·	1.0	•		5
33.4	1.0	•		35.2
32.0	1.0		<0.1	
8.	1.0			35.0
28.0	0.9			
33.8	1.0		<0.1	4.
33.9	1.0		<0.1	
32.7	1.0		<0.1	
35.4	1.1			
	0.9	• '	<0.1	34.6
4.	1.1	•	<0.1	
·	_ _	•		4



Ratios ov	er Backgro	an pan	Compar IGER/IR	isons isons
1	1	1	•	•
سو	1.0		<0.1	34.2
سو	1.0	•	<0.1	•
$\sim$	1.0	•		33.9
N	1.0	•	0	•
w	1.0	•	<0.1	33.7
w	1.0	•	0	ω.
$\vdash$	1.0	•	0.	•
w	1.0	•	0	Ü
w	1.0	•	0	u
σ	1.0	•	0.	u
w	1.1	•	0	w
9	1.2	•	0	w
w	1.1	•	0	w
. <b>~</b> 1	1.0	•	0	Ν
J	1.2	•	0	2
32.3	1.1	34.6	<0.1	32.6
_	1.0	•	0	N
w	1.1	•	0	-
0	1.1	•	<0.1	-
ø	1.0	•	<0.1	-
_	0.9	•	0	9
'VO	1.0	•	0	8
N	0.9	4.	<0.1	6
an.	1.0	ŗ	•	6.
	1.0		•	4.
5	1.0	w	•	ω ·
3.5	1.1	•	0.2	



HLCVLEDELWGVSLFGYCSS	F815-3-H1-IGFR
HQCI PDGMSQGAALRGNCSD	F815~4-G12-IGFR
QRCIRAALFWCATLLGGCAG	F815-3-G1-IGFR
HLCVLVGLFWDASLFGQCSG	F815-3-B3-IGFR
FLCGLEELSQGAVLFGHCYG	F815-4-A10-IGFR
FYCGLEELSWGAALFGYCSG	F815-4-G7-IGFR
RVCVLEQLVWGASLFGA*SG	F815-4-E7-IGFR
FLCGLQELSGVASLFGQCSG	F815-4-C7-IGFR
QLCVLE#LFWGACLFGYCAG	F815-4-C11-IGFR
PLCVLQELFGGGSLGGYCSG	F815-4-D12-IGFR
PLCFLAELFSGSALGGDCSR	F815-3-B5-IGFR
FLCGLEELAWGVSRSGYCFG	F815-4-B7-IGFR
PLCFLQELFGGGSLSGYCSG	F815-4-H10-IGFR
FMCGLQELVGGAALLGHCSG	F815-4-E12-IGFR
PLCFLQELFGGASLGGYCSG	F815-4-F11-IGFR
HLCVLEELFWGASLFGYCSG	Parental/Design
Sequence	Clone

18.4	7.6	20.5	7.6	30.8	30.4	26.9	16.8	13.9	33.6	33.9	35.2	30.1	33.7	33.4	39.1	Ę-Tag	Ratios ov
1.0	1.0	1.0	1.0	3.7	9.0	3.8	2.0	4.6	7.0	4.8	23.9	8.5	15.1	12.3	1.8	IGFsR	er Backgro
6.8	_	_	-		5.0	1.9	1.0	1.8	1.8	1.0	4.8	1.0	1.7	1.0	27.7	R	bund
	0.4				1.8	2.0	2.0							12.3			Compa
						0.5							0.1	0.1	15.4	IR/IGFR	risons

F820-4-A11-IR F820-4-E8-IR F820-4-H3-IR	F820-4-F5-IR F820-4-F12-IR	20-4-F1-I 20-4-A3-I	F820-4-F4-IR F820-4-B10-IR F820-4-A5-IR F820-4-F6-IR	20-4-H8-I 20-4-D7-I 20-4-B2-I 20-4-C3-I		Clone Parental/Design F820-4-B5-IR F820-4-A2-IR F820-4-E2-IR F820-4-D10-IR F820-4-H7-IR F820-4-G6-IR F820-4-C2-IR
HLCGMEEMFWGVALFRNCSG PLCVLEQLYWGESLFVYCSG HLCLLEELFWGEALWGYCSG	QLCVLEELYWGASLFGHCSG HLCVLEDRFWGASLFGPCSG	CVLEEMFWGTSHFDGCS CVLEELFWGAPLFGLCS	PLCVLEELYWGAALFGDCYG PLCVLEELFWGLSLDKNCS QLCVLEELFWGASLFSGCSG PLCDLEALFWGESLFGGCSG		SQCT GSCS RDCP RQCS	Sequence HLCVLEELFWGASLFGYCSG HLCMLEEQFWGASLFSRCSG TCAFWKNGSGVRRCSVTAVV PLCGLKN.SGVRLCSSPALV PLCLQEELFWGASLFGYCSG PLCDLEELFWGASLFGDCPG DLCVLEELFWDGSLFASCSG PLCVLEEQLWGTALFGSCTG

Figure 4D				Y
		y.		
	7.5 5.3 5.7 9.1 5.9 25.7 3.7 11.3 7.6 8.0	38.1 15.1 46.3 14.5 8.8 11.7 16.0 14.5 5.0 37.5	Ratios ov E-Tag 39.1 28.1 34.0 21.3 34.1 14.2 14.0	
	21.06.68 2.60.68	1.2 0.6 0.6 0.6 1.1	ver Backgrou IGFsR 1.8 0.9 1.6 0.7 0.7 0.6 0.5	
	10.5 4.4 2.7 2.7 9.0 9.0	11 22 64 64 64 64 64 64 64 64 64 64 64 64 64	IR 27. 17. 22. 22. 9. 12. 6. 6.	
	00000000000			
		9. 5.6.77.38.00 7.34.50 7.96.91	IR/IGFR 15.4 21.1 13.9 13.4 12.1 11.6 11.6	

Clane	Semience
Parental/Design	HLCVLEELFWGASLFGYCSG
F820-4-A8-IR	QLCVMEELFWGASRFGQCSG
F820-4-G1-IR	HLCVLEELFWGASMFGQCSG
F820-4-F3-IR	QLCVLEEMFWGGSRFVQCSA
F820-4-D6-IR	PLCILEELFWGEALFDQCGA
F820-4-A1-IR	YLCVQEELFWGASLFGYCSV
F820-4-H2-IR	HLCALEEAFFGPSLFNSCQG
F820-4-F4-IR	HLCVLEERFWGASLFGQCSG
F820-4-B6-IR	QLCDLEELFWGASLFGYCPG
F820-4-B11-IR	<b>HLCVLEERFWGASIWGSCSG</b>
F820-4-H6-IR	QLCVLEELFWGGSLWGQCSR
F820-4-H9-IR	PLCVLEELFWGAAQFGQCSG
F820-4-D3-IR	QLCDLEERFWGVSLFGLCSG
F820-4-C1-IR	QLCVLEEVFWGASLFGLCTG
F820-4-D12-IR	QL.DLNTWSGLCLCSVTVRV
F820-4-B8-IR	DLCVLEESLWGKALFGYCSD
F820-4-C6-IR	HLCVLEEVFWGSSMFGDCSG
F820-4-C10-IR	HLCDLEELFWGASLFGDCQG
F820-4-D4-IR	QLCVLDALMWGGCRLGHQCG
F820-4-E1-IR	QLCVLEEKFWGTSLFGDCMG
F820-4-B3-IR	HLCVLEEVFWGAAQFGSCSG
F820-4-D2-IR	QLCVLEELFWGPSMFGYCSG
F820-4-C5-IR	HLCDLEELFWGASGFAQCYG

Ratios ov	ver Backgro	H Āuiģ	Compai	risons IR/ICFR
	1 ,	:	: .	
	0.7	2.4	0.3	w
9	0.6	1.9	0.3	w
œ	1.3	3.6	0.4	2
4	1.2	3.2	Q.4	2
5	2.4	6.1	0.4	2
9	1.6	4.1	0.4	2
œ	1.9	4.7	0.4	2
_	0.8	1.9	0.4	2
N	3.1	7.0	0.4	2
-	1.1	2.4	<b>0.5</b>	2
-	0.9	1.9	0.5	2
6	1.3	2.5	0.5	
0	1.1	2.1	0.5	1
4	1.2	2.0	0.6	1
N	2.2	3.4	0.6	1.
9	2.5	2.8	0.9	1.
w	2.6	2.9	0.9	
S	2.3	2.1	1.1	0.
9	1.6	1.5	1.1	0.
9	0.6	5.0	1.2	0.
æ	3.2	2.5	1.3	0.
ഗ	4.0	2.3	1.8	0

Sequence
VLEELFWGA
<b>DLCVLEERFWGASLFGQCSG</b>
/LEELHWGASLFG
YLCDLEERFWGASLFGQCSS
HLCLLEERFWGSSQFGFCSG
HLCVLEELFWGASQFGQCSG
HLCYLEERFWGASLFGQCSG
HLCVMEELFWGTSLFGQCTG
HLCVLEERFWGASLFGQCSG
HLCVLEERFWGASLFSQCSG
HLCVLEELFWGASLFGQCSG
QLCLLEELFWGAASFGQCSG
HLCVLEEMFWGASLFGQCSG
HLCDLEELFWGASLFSQCSR
QLCVLEELFWGASQFGYCSG
<b>QLCALEEQFWGASLFSQCSG</b>
QLCVLEELFWGASLFGYCSG
HLCVLEEWFWGDSLFGQCSR
HLCVLEERFWGASLFGQCSG
QLCELEEVFWGASLFDYCSG
HLCVLEELFWGASRFGQCSG
HLCVLEELFWGASLFGQC\$A
HĻCVLEELIWGASRFGQCSG
HLCVLEELFWGGSLF1QCSG
QLCVLEEQFWGASLFGNCSG
HLCVLEERFWGAALFGQCSG
HLCILEEMFWGASLFGQCGG
PLCVLEELVWGASLFVQCSG

Ratios ove	er Backgro	hud	Compari	risons	
E-Tag	<b>IGFsR</b>	₹	<b>ICFR/IR</b>	IR/IGFR	
:	1	:	1	;	
36.9	1.0	40.5	<0.1	42.5	
38.6	1.0	40.1	<0.1	40.7	
39.6	1.1	44.8	<0.1	40.6	
37.3	1.0	40.3	<0.1	40.3	
•	1.1	44.4	<0.1	40.2	
26.7	1.1	42.2	<0.1	40.2	
•	0.9	36.9	<0.1	. 39.8	
33.9	1.0	38.7	<0.1	39.3	
•	1.1	٠	<0.1	•	
38.1	1.1	42.7		37.7	
•	1.1	•	<0.1	•	
38.5	1.1	41:1	<0.1	36.5	
٠	1.1	39.7		36.2	
•	1.0	7.		36.1	
•	1.1	8		35.8	
37.4	1.2	40.5	<0.1	34.8	
0	1.0	Š	<0.1	34.3	
4	1.2	40.2	<0.1	33.7	
34.4	1.2		<0.1	33.2	
4.	1.2	39.6	<0.1	•	
	1.2	•		31.7	
32.3	1.2	37.4	< 0.1	30.6	
•	1.1	33.3		30.2	
•	1.3	40.3	<0.1	30.1	
36.4	1.4	39.8		29.3	
	1.1	•	<0.1	29.2	
34.0	1.4	38.8		•	
9	1.2	2	<0.1	8	

B6C-4-E10-IR HL	20C-3-A7-IR FLC	20C-3-A8-IR HL	20C-3-B12-IR <u>Q</u> L	20C-4-E1-IR <u>Q</u> L	20C-4-F1-IR HL	20C-3-A10-IR HL	20C-3-B1-IR HL	B6C-3-C5-IR HL	20C-3-A9-IR	B6C-4-E4-IR NL	20C-3-A6-IR HL	20C-3-A4-IR HL	20C-3-A11-IR EL	20C-3-C2-IR HL	20C-3-C3-IR RL	20C-3-C12-IR LL	20C-3-B3-IR HL	20C-3-B11-IR HL	20C-3-A5-IR QL	A6L-3-B3-IR PL	A6L-3-A3-IR HL	20C-3-B6-IR HL	20C-3-C10-IR HL	20C-3-B8-IR HL	B6C-4-G2-IR HL	20C-3-C11-IR HL	₿4 - IR	Design HL	Clone Sec	
HLCVLEEQFWGASLFGYCSG	£	HLCVLEELFWGASLFG <u>O</u> CSS	LCGLEELFWGASLFGYCSA	QLCVLEELFWGTSLFAGCSG	HLCDLEELFWGASLFGQCSG	CVLEERFWGGALFGQCTA	HLCVLEVQIWGASLFGQCSG	CVLEEQFWGVALFGNCSG	PLCVLEEQLWGASLFRYCSG	NLCVLEELFWGASEFGOCSG	HLCVLEELFWGASLFAQCPG	HLCVLEELFWGASLYGQCSS	ELCFLEELFWGASLFG <u>Q</u> CSG	HLCVLEEMFWGASLFGNCSG	CVLEELFWGESLFGQCSG	LLCVLEEQFWGASLFGQCSG	<b>HLCVLEELVWGÄSLFGFCSG</b>	CVLEELFWGQSLFGHCSD	QLCVLEETFWG\$SLFAQCLG	PLCVLEEQFWGASLFAYCSS	HLCVLEEQYWGESLFGYCSG	HLCVLEERFWGASLFWQCSG	HLCVMEELFWGASLFGQCSG	<b>HLCDLEVLFWGSALFGQCSG</b>	CFLEEVFWGAALFAQCSG	HLCVLEEQFWGGSLFGYCSR	NLCVLEELFWGESLFGQCSG	HLCVLEELFWGASLFGYCSG	Sequence	

		,
0 2 2 2 3 3 3	30.0 29.3 30.1 29.9 25.9 27.2 26.1 34.5 39.7 29.7	
2.1.3.4	1.27.3	er Backgrou IGFsR 1.1 1.3 1.3 1.1 1.2 1.2 1.2 1.2
29.5 29.7 25.8 21.2 23.0	32.7 31.8 30.1 29.8 27.4 27.5 27.5 27.5 29.3 39.1 29.3	31.1 31.0 35.3 31.2 31.2 31.2 31.2 31.9 28.3
0.1 0.1 0.1		0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
	25.8 24.8 24.3 23.8 23.0 22.9 22.9 22.7 22.7 22.7 22.7	1 0 0 0 0 7 7 7 7 0 1 C

Clone	Sequence
<b>Design</b>	HLCVLEELFWGASLFGYCSG
20C-3-A1-IR	RLCALEELFWGASLFGQCSG
20C-3-C1-IR	HLCVLEELFWGAALFHQCSG
A6L-3-D2-IR	RLCVLEEQFWGASLFGQCSG
B6C-4-G12-IR	QLCVLEELFWGSSRLGYCSG
B6H-4-F9-IR	DLCVLEELFWGASLFGQCSG
B6C-4-E3-IR	QLCLLEEQFWGGSLFGQCSG
20C-3-B10-IR	HLCVLEELFWGTSLFGQCSG
20C-3-A3-IR	RLCVLEELVWGASLFDQCSR

Ratios ov	Ratios over Background	ųnd	Comparisons	risons	
E-Tag	<b>ICFsR</b>	₹	IGFRIR	IR/IGFR	
:	:	:	;	•	
21.0	1.1	17.6	0.1	16.6	
30.6	1.4	21.9	0.1	16.1	
7.0	1.1	14.9	0.1	14.1	
31.1	2.5	33.5	0.1	13.6	
39.3	3.6	43.1	Q.1	12.1	
34.6	· σ . ω	40.0	0.1	7.6	
29.9	16.9	31.7	0.5	1.9	
28 4	191	20	0	_	

Clone	Sequence
Parental/Design	HLCVLEELFWGASLFGYCSG
F815-4-D10-IGFR	PLOALCERFFGAWMFGYCSG
F815-4-H11-IGFR	HLQVLCELFGGVYLFGYCSG
F815-4-C8-IGFR	PLFDLCELFGGASLSGYCYG
F815-4-E8-IGFR	HL*ALCELFGGVWSFGYCVG
F815-4-E11-IGFR	QLGVLCEMFGGAFRLGYCQG
F815-4-A7-IGFR	HLQDLCELFGGAYLFGYCSG
F815-3-D3-IGFR	QLQVLCELFGGAVSLRLLLW
F815-4-F7-IGFR	PLGVLCEQFGGAFRFGYCSG
F815-4-A9-IGFR	PL*GLCELFGGASLFGYCSS
F815-4-B12-IGFR	DLRVLCELFGGAYVLGYCSE

Ratios over	er Backgro	und	Compa	risons	
E-Tag	IGFsR	≅	IGFIVIR	IRIGER	
39.1	1.8	27.7	0.1	15.4	
31.2	13.9	1.0	13.9	0.1	
27.2	19.2	1.7	11.3	0.1	
35.4	17.4	1.6	10.9	0.1	
29.5	16.9	1.7	9.9	0.1	
36.6	25.7	2.7	9.5	0.1	
29.6	16.0	3.8	4.2	0.2	
33.7	3.5	1.0	3.5	0.3	
33.6	18.9	9.9	1.9	0.5	
7.5	1.7	2.3	0.7	1.4	
36.1	٦. ٦	12 6	0.3	٠. 4	

Clone	Sequence
)esign	XXXXXXXXXXXXXXXXXX
₹20α-3-20A4-IR	EIEAEWGRVRCLVYGRCVGG
₹20 }-4-A7-IR	<b>EIEAEWGRVRCLVYGRCVGG</b>
\20β-4-D8-IR	WLDQEWAWVQCEVYGRGCPS

_	_				
<b>etios</b> ove	E-Tag	:	50.2	44.2	•
Ratios over Background	<b>I</b> GFsR	1	1.6	1.3	
ģnţ	₹	:	23.1	24.0	) }
Comparisons	ICFIVIR IR/ICFR	1	0.1	0.1	•
risons	IR/IGFR	•	14.4	18.5	נ נ

	D815-4-F7-IR
CT	D815-4-H11-IR
SLDQEWAWVQCEVYGRGCLS	D815-4-A7-IR
WLEQEWAWVQCEVYGRGCLS	D815-4-H12-IR
WLDQEWAVMKCELYGRGCPS	D815-4-F11-IR
WLDQEWAWVRCEVYGLGCPS	D815-4-C9-IR
	D815-4-H10-IR
QLEQEWAWVRCEVYGRGCSS	D815-4-C7-IR
DHE * AWVOCEVYGRGCP	D815-4-A10-IR
QLDQEWAWVLCKVYGRGCPS	D815-4-F9-IR
EWAWVECQ	D815-4-E8-IR
EWAWVECEVYGRR	D815-4-F12-IR
EVYGRG	D815-4-H7-IR
WLDQEWAWVQCEVYGRGCPS	D815-4-E11-IR
WLDQEWALVQCEVYGRGCPS	D815-4-G12-IR
WLEEEWAQVQCAVYGRGCSS	D815-4-G9-IR
WLEQEWĄQVQCEVYGRGCRS	D815-4-D7-IR
SLDKEWEWVLCVVYGRGCPS	D815-4-E10-IR
WLDQEWAGVLCEVYGRGCPS	D815-4-H8-IR
WLDQEWAWVQCEVYGRGCPY	D815-4-B10-IR
WLEQEWEQVRCLVYGRGCPP	D815-4-E9-IR
SLOWEWAWLQCEVYGRGCPS	D815-4-A9-IR
WLDQEWAWIQCEVYGRGCPA	D815-4-F8-IR
WLEQEWAWVQCEVYGRGCQS	D815-4-D12-IR
WLDEEWEWIQCKVYGRGCPA	D815-4-D11-IR
WLEQEWAQVQCEVYGRGCPS	D815-4-B7-IR
WLEQEWAWIQCEVYGRGCPS	D815-4-E12-IR
RLDEEWARVQCEVWGRGCRS	D815-4-All-IR
WLDQEWQQVQCQVYGRGCTS	D815-4-D9-IR
WLDQEWAQVQCEVFGRGCPS	D815-4-D10-IR
<b>WLDLEWAQVQCEVYGRGCPS</b>	D815-4-A8-IR
WLDQEWAWVQCEVYGRGCPS	Par ntal/Design
Sequence	Clone

32.4		្ស	40.4	44.2	47.0	37.7	•			•		•	•		•	•	•	•	47.8	•	47.8	48.1	49.5	.45.4	49.0	47.9	47.5		48.0	44.8	E-Tag	Ratios ove
1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.4	IGFSR	r Backgro
34.7	2 <del>-</del> 7	38.6	•	39.8	39.8	•	•	•	42.6	•	•	•	43.7		45.4	ა	45.6	•	•	•	46.4	•	47.0	•	•	•	•	•	48.4	24.2	₹	pnų
<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	IGFIVIR	Compa
34.7	7	38.6	39.2	39.8	39.8	40.0	41.2	41.8	42.6	42.6	43.0	43.0	43.7	44.2		45.6	45.6	45.6	45.8	45.8	46.4	46.6	47.0	47.2	47.6	48.0	48.0	48.2	48.4	17.3	RIGER	risons

Clone Parental/Design D815-4-G8-IR D815-4-G7-IR D815-4-G11-IR D815-4-E7-IR D815-4-A12-IR	Scquence  MLDQEWAWVQCEVYGRGCPS  QLDÖEWARVRCEVWGRGCPS  WLDLEWAQVQCKVYGRGCPS  WLDEEWAWVQCQVYGRGCPS  WLDEEWAWVQCEVWGRGCPS  WLDQEWAWVQCEVWGRGCAF
Q815-4-G11-IR	WLDEEWAWVQCQVYGRG
D815-4-E7-IR	WLDQEWAWVQCEVWGRG
D815-4-A12-IR	WLDREWAQVQCEVYGRGCLS
D815-4-B11-IR	WLDAEWEWVQCEVYGRGCRP
D815-4-D8-IR	SLDREWAYVQCQVYGRGCSS

Ratios ov	Ratios over Background	ģnų	Comparisons	sons	
E-Tag	IÇFsR	Ħ	IGFR/IR IR/IGFR	VIGFR	
!	:	;	:	!	
27.8	1.0	33.6	<0.1	33.6	
34.7	1.0	32.3	<0.1	32.3	
30.7	1.0	28.6	<0.1	28.6	
33.0	1.0	26.4	<0.1	26.4	
28.4	1.0	19.0	0.1	19.0	
22.1	1.0	18.8	0.1	18.8	
20.8	1.0	14.6	0.1	14.6	

Ratios ov E-Tag 44.8 23.9 31.0 35.2 33.8	er Backgro IGFsR 1.4 1.0 1.0 1.0 1.0	und IR 24.2 40.0 39.5 39.4 38.8	Compa IGFR/IR 0.1 <0.1 <0.1 <0.1	IR/IGFR 17.2 40.0 39.5 39.4 38.8
	1.0			39.4
•	1.0	•		•
	1.0	•	<0.1	37.8
	1.0	•	<0.1	•
	1.0		<0.1	37.1
4.	1.0	•	<0.1	•
•	1.0	•	<0.1	•
<u>-</u>	1.0		<0.1	٠
2	1.0		<0.1	6.
'n	1.0	• .	<0.1	5.
φ.	1.0		<0.1	5.
0	1.0	34.8	<0.1	•
9	1.0	•	<0.1	4
0	1.0	ú	<0.1	·
31.3	1.0	33.0	<0.1	33.0
0	1.0	•	<0.1	•
8	1.0	•	<0.1	•
w	1.0	0	<0.1	•
29.1	1.0	0	<0.1	30.3
5	1.0	9	<0.1	29.5
6	1.0	8		28.6
4.	1.0	6		26.0
23.7	1.0		<0.1	•
2	1.0			5
2	1.0	Ü		23.9
	1.0	N		2

Clone	Sequence
Parental/Design	WLDQEWAWVQCEVYGRGCPS
D820-3-Ę5-IR	WLEĞEWTWVQCEVYGÇÇÇPS
₽820-3-₽1-IR	WLEKEWAGVQCE I YGRGCPS
D820-3-E1-IR	WLEEEWAWVRCEVYGRGCQS
<b>D820-3-F1-IR</b>	WLEHEWAQIQCELYGRGCTY
₽820-3-B2-IR	<b>ALEEEWAWVQCEVYGRGCPS</b>
<b>D820-3-A3-IR</b>	WLEQEWAQVQCEVYGRGCPS
D820-3-H4-IR	WLDDEWAQIQCEIYGRGCQS
D820-3-G1-IR	QLEEEWAGVQCEVYGRECPS
D820-3-C1-IR	WLEQEWLLVQCGVYGRGCPS
D820-3-A1-IR	WLDQEWAWIQCEVYGRGCRS
D820-3-A5-IR	WLEQEWAQVQCEVSGRGCPS
D820-3-H1-IR	W?DQEWALIQCEVYGRGCPS
<b>D820-3-A4-IR</b>	SLDEEWAGVLCEVYGRGCPF
D820-4-E12-IR	SVDQELEWLMCHFQGRVCPS
D820-4-B12-IR	WLEQERAWIWCEIQGSGCRA

32.2	34.9	6. þ	13.7	6.4	14.7	27.8	14.5	25.6	23.5	13.1	22.0	22.4	27.3	25.9	44.8	E-Tag	Ratios ov
8.6	9.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.4	<b>ICFsR</b>	er Backgro
1.0	10.9	4.3	6.2	6.3	12.8	13.9	16.3	17.5	18.4	18.4	21.0	21.9	22.4	22.6	24.2	₹	pand
8.6	0.8	0.2	0.2	0.2	0.1	0.1	0.1	0.1	0.1		<0.1	<0.1	<0.1	<0.1	0.1	<b>ICFIVIR</b>	Compa
0.1	1.2	4.3	6.2	6.3	12.8	13.9	16.3	17.5	18.4	18.4	21.0	21.9	22.4	22.6		<b>IIVIGER</b>	risons

Clone	Sequence
Parental/Design	WLDQEWAWVQCEVYGRGCPS
D820-3-D5-IGFR	WVNQAĻGGVQSDVQGRRCQS
D820-3-E4-IGFR	LLDHEWPWVGCEVCGRGSLS
D820-3-C5-IGFR	WLHQELAWVRGEGYPRGRRS
D820-3-F4-IGFR	MLGHDWAWIQCEVYGLGCPC
D820-3-F6-IGFR	WIDQEGVRVQCEA*GRAFPS
D820-3-G4-IGFR	WRDEEWAWVQGVVQGRGWPA
D820-3-E2-IGFR	RLGVEWSWFQRKVYGRDSTS
D820-3-G6-IGFR	WLAQGWAGVQCVVYGRGCRN
D820-4-E11-IGFR	WLEEE * AGIQCQV?GRGCPS
D820-4-H11-IGFR	WLDQEWEWVQCEVWGRGCLS
D820-4-D11-IGFR	RLEQEWALIQCEVYGRGCPS
D820-4-A8-IGFR	WLEEEWAQVQCQVYGRGCAS
D820-4-F9-IGFR	WLDLE*EWLQCEVYGRGCAT
D820-4-C8-IGFR	WLEQEWVQVRCEVYGRGCPS
<b>D820-4-D9-IGFR</b>	WLEEEWAQVQCEVYGRGCPS
<b>D820-4-D7-IGFR</b>	WLDQEWARVQCEVWGRGCTY
D820-4-H9-IGFR	YLD?EWAWVQCEVYGLGCQS
D820-4-E10-IGFR	WLDVE*AWVQCEVWGRGCPS
D820-4-E7-IGFR	WLEQEWER?QCEVYGRGCPP
D820-4-H8-IGFR	WLEEEWAQVQCEVYGRGCLS
D820-4-A11-IGFR	WLDQEWAWIQCEVYGRGCPS
D820-4-C9-IGFR	?LEHEWAQIQCEV?GRGCQS
D820-4-E9-IGFR	WL?QEWAWIQCEVYGRGCPF
D820-4-B10-IGFR	WLD?EWAWVQCEVYGRGCPS
D820-4-F10-IGFR	GLEQGCPWVGLEVQCRGCPS
D820-4-B9-IGFR	WLEEEWAWVQCEVYGHGCPS
D820-4-G8-IGFR	WLDQEWAQIQCEVYGRGCSS

25.6	31.7	27.8	19.3	19.3	19.6	8.0	16.1	31.9	26.7	18.4	34.1	10.1	11.6	9.4	3.2	4.5	8.1	12.6	20.3	15.3	3.8	26.7	ω.	25.0	7.	29.6	44.8	E-Tag	Ratios ove
1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	3.0	2.6	1.0	3.5	1.0	1.0	1.0	1.0	1.0	1.0	1.0	2.4	2.6	2.6	2.6	2.7	3.1	3.2	3.8	1.4	<b>IGFsR</b>	er Backgro
29.3	26.5	25.7	21.5	17.3	14.9	12.5	11.7	32.2	27.0	10.1	33.4	8.9	5.9	5.8	5.5	5.3	4.6	3.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.φ	24.2	R	pnů
	<0.1	<0.1	<0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.2	0.2	0.2	0.2	0.3	2.4	2.6	2.6	2.6	2.7	3.1	3.2	3.8	0.1	IGFR/IR	Compa
•	26.5	•	•	•	•	•	11.7	10.7	10.4	10.1	-	8.9	5.9	5. Ą	5.5	5.3			0.4			0.4		ě	Q.3	0.3	17.3	IR/ICFR	risons

4.	-4-A7-	-4-C12	D820-4-A12-IGFR	D820-4-D12-IGFR	D820-4-G12-IGFR	D820-4-F7-IGFR	D820-4-F12-IGFR	D820-4-H10-IGFR	D820-4-E12-IGFR	D820-4-B7-IGFR	D820-4-A10-IGFR	D820-4-D8-IGFR	D820-4-D10-IGFR	D820-4-G10-IGFR	D820-4-E8-IGFR	D820-4-H7-IGFR	D820-4-F8-IGFR	D820-4-B8-IGFR	D820-4-A9-IGFR	D820-4-C10-IGFR	D820-4-G9-IGFR	Parental/Design	Clone
SLEHE*AWVQCKVYGRGC?S	RLEOEWAWIOCEVYGRGCRF	OLELEWARVOCEVWDRGCPS	CLDQEWA?VQCPVYGRGCPS	WLEEE*GWVQCEVWGRGCPP	WLEEEWAQIRCGVYGRGCPS	LGDQEWAWVEWEV#GRGWPS	SLDKEWAWVKCEVYGRGCPS	WLDQEWVRVQCEVWGRGCPS	SLE?EWAWVQCEV?GRGCP?	PLEHEWAWVQCVVYGRGCRS	WL?QEWARVHCEVWGRP?QC	WLEQE*ARVQCEVWGRGCPS	WLEQEWAQVQCDVYGRGCPS	WLE?EWEWVQCEVYGRGC?S	WLEQEWAQIQCEVWGRGCSS	WLEQEWALVLCEVYGHGCPA	WLEQEWAQIQCQIYGRGCPS	WLDLEWEQIKCKVYGRGCPF	WLEQEWASVQCEVYGRGCPS	WLDLEWEFVQCEVYGRGCPT	WLDQEWAQVQCEVWGRGCPS	<b>WLDQEWAWVQCEVYGRGCPS</b>	Sequence

36.2	35.4	37.1	30.4	37.2	30.3	34.4	36.9	36.8	37.0	35.4	29.4	23.7	36.6	37.5	26.6	34.1	28.3	31.1	20.4	32.6	36.8	44.8	Ę-Tag	Ratios ov
1.0	1.0		1.0		1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.4	<b>IĢFsR</b>	er Backgro
41.4	40.8	9	9	8	7	7	7	7	37.0	σ	5	4	w	w	w	Ν	2	N	$\mathbf{\vdash}$	31.3	•	4	≅	und
<0.1	•	<0.1	0	0	0	0	0	0	<0.1	Ō	0	0	0	0	0	0	<0.1	<0.1	<0.1	<0.1	?	0.1	IGFR/IR	Compa
41.4	40.8	9	9	æ	7	7	7	7	37.0	9	S	4	w	w	w	Ν	Ν	Ν	-	$\boldsymbol{\vdash}$	9	7	IR/IGFR	risons

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1	2
1	2
1	Ξ
-	п

Parental/Design II B6-4-G12-IR II B6-3-A11-IR

Sequence
IR/IGFR
MLDQEWAWVQCEVYGRGCPS
WLDQEWAWIQCEVYGRGCPP
WLDQEWAQVRCEVYGRGCPS

## Ratios over Background Comparisons E-Tag | IGFSR | IR | IGFR/IR 44.8 | 1.4 | 24.2 | <0.1 | 17.3 | 44.4 | 1.0 | 6.9 | 0.1 | 7.1

	Sequence	HIR affinity mol/l
J228	HPPLEHLKAFLL-NH2	2.4*10-5
J229	APTFYAWFNQQT-NH₂	2.4*10-6
S122	HPTSKEIYAKLLK	9.3*10-6
S123	HPSTNQMLMKLFK	1.6*10-5
\$124	HPPLSELKLFLIKK	2.3*10-5

Figure 7

J-nr	Sequence	HIR affinity mol/I
J101	ACVWPTYWNCG	5.0*10 <sup>-6</sup>
J103	Ac-CVWPTYWNCG	3.0°10 <sup>-5</sup>
J104	Bz-CVWPTYWNCG	3.2*10 <sup>-5</sup>
J105	Ac-ACVWPTYWNGG	4.5*10-5
J109	ACVWPTYWACG	2.0*10-5
J110	ACVWPTYANCG	2.4°10 <sup>-5</sup>
J111	ACVWPTAWNCG	3.1°10 <sup>-5</sup>
J112	ACVWPAYWNCG	3.3°10 <sup>-5</sup>
J113	ACVWATYWNCG	5.5*10 <sup>-5</sup>
J115	ACAWPTYWNCG	2.7*10 <sup>-6</sup>
J116	AAVWPTYWNAG	3.4*10 <sup>-5</sup>
J117	ASVWPTYWNSG	2.9*10 <sup>-5</sup>
J118	ACPYNWVTWCG	2.9°10 <sup>-5</sup>
J119	ACVWPTYWnCG	3.2°10 <sup>-5</sup>
J120	ACVWPTYWNCG	3.4*10 <sup>-5</sup>
J121	ACVWPTyWNCG	1.8*10 <sup>-5</sup>
J122	ACVWPtYWNCG	5.1°10 <sup>-5</sup>
J123	ACVWpTYWNCG	2.5°10 <sup>-5</sup>
J124	ACVWPTYWNGG	2.0*10-5
J125	ACVWPTYWNCG	1.8*10-5
J127	acvwptywncg	4.4*10-5
J128	gcnwytpwvca	5.3°10 <sup>-5</sup>
J130	AEVWPTYWN(Dpr)G	1.9*10-5
J131	ACDWPTYWNCG	5.5*10-5
J132	AC(Leu)WPTYWNCG	4.5*10-6
J133	AC(dLeu)WPTYWNCG	2.8*10 <sup>-5</sup>
J134	AC(IIe)WPTYWNCG	7.4*10 <sup>-6</sup>
J135	AC(dlle)WPTYWNCG	2.9*10-5
J136	AC(Met)WPTYWNCG	7.5*10-6

FIGURE 8



		<u> </u>
J137	AC(dMet)WPTYWNCG	2.5*10 <sup>-5</sup>
J138	AC(Abu)WPTYWNCG	7.8°10 <sup>-5</sup>
J139	AC(dAbu)WPTYWNCG	2.1*10-5
J140	AC(Nva)WPTYWNCG	3:6°10 <sup>-6</sup>
J141	AC(dNva)WPTYWNCG	3.0*10-5
J142	AC(tBuG)WPTYWNCG	3.2*10-5
J143	AC(dtBuG)WPTYWNCG	3.8*10-5
J144	AC(Phe)WPTYWNCG	5.1*10 <sup>-6</sup>
J145	AC(dPhe)WPTYWNCG	5.7*10-5
J146	AC(Cha)WPTYWNCG	2.2*10-5
J147	AC(dCha)WPTYWNCG	1.7*10-5
J148	AC(Nal(1))WPTYWNCG	5.8 <b>*</b> 10 <sup>-6</sup>
J149	AC(dNal(1))WPTYWNCG	2.0*10-5
J150	AC(Acy)WPTYWNCG	2.0*10-5
J151	ACVWPT(Hyp)WNGG	2.2*10-4
J154	ACVWPT(Nal2)WNCG	8.2*10-5
J155	ACVWPT(MetO <sub>2</sub> )WNCG	1.9*10-4
J157	ACVWPT(Cha)WNCG	1.2*10-4
J160	ACVWPT(Ser)WNCG	1.8*10-4
J162	ACVWPT(Thi)WNCG	2.5*10-4
J163	ACVWPT(dSer)WNCG	5.0°10 <sup>-5</sup>
J166	ACVWPT(dCha)WNCG	7.5*10 <sup>-5</sup>
J170	ACVWPT(dPhe)WNCG	1.4*10-4
J171	ACVWPT(Thr)WNCG	7.7*10-4
J174	ACVWPT(Phe)WNCG	4.5°10 <sup>-5</sup>
J176	ACVWPT(dThr)WNCG	2.8*10-5
J180	ACVWPTYW D CG	5.6*10 <sup>-5</sup>
J182	ACVWPT D WNCG	2.7*10 <sup>-5</sup>
J183	ACVWP b YWNCG	3.3*10 <sup>-5</sup>
J184	ACVW D TYWNCG	6.2°10 <sup>-5</sup>

Figure 8 (Con't)



J185	ACV D PTYWNCG	3.4°10 <sup>-5</sup>
J186	AC D WPTYWNCG	3.5°10 <sup>-5</sup>
J187	ACVWTYWNPCG	4.3°10 <sup>-5</sup>
J188	ACVWTYWPNCG	3.0°10 <sup>-5</sup>
J189	ACVWTYPWNCG	3.1°10 <sup>-5</sup>
J190	ACVWTPYWNCG	2.6°10 <sup>-5</sup>
J191	ACVPWTYWNCG	3.0°10 <sup>-5</sup>
J192	ACPVWTYWNCG	4.2*10 <sup>-5</sup>
J193	ACWPTYWNVCG	4.8*10 <sup>-5</sup>
J194	ACPTYWNVWCG	4.2*10-5
J195	ACTYWNVWPCG	3.3*10 <sup>-5</sup>
J196	ACYWNVWPTCG	2.4°10 <sup>-5</sup>
J197	ACWNVWPTYCG	2.9*10 <sup>-5</sup>
J198	ACNVWPTYWCG	4.2°10 <sup>-5</sup> ·
J199	ACVWPCG	4.7°10 <sup>-5</sup>
J200	CVWPTYWNCG	5.5*10 <sup>-5</sup>
J201	ACWWPTYWNCG	6.8 <b>*1</b> 0 <sup>-6</sup>
J202	ACEWPTYWNCG	4.6*10 <sup>-6</sup>
J203	ACRWPTYWNCG	5.8*10 <sup>-6</sup>
J204	ACQWPTYWNCG	9.2*10 <sup>-6</sup>
J205	ACGWPTYWNCG	4.4*10 <sup>-6</sup>
J207	cyclo-Valeroyl-AWPTYWNCG	5.5*10 <sup>-5</sup>
J208	cyclo-Toluyl- AWPTYWNCG	7:6*10 <sup>-5</sup>
J209	cyclo-Acetyl- AWPTYWNCG	7.7°10 <sup>-5</sup>
J210	(WPTYWNCG) <sub>2</sub>	5.3*10 <sup>-5</sup>
J211	(AWPTYWNCG) <sub>2</sub>	7.9 <b>*</b> 10 <sup>-6</sup>
J212	ACA(Bpa)PTYWNCGK(biotin	1.8*10-5
J213	ACAWPTY(Bpa)NCGK(biotin	1.8*10 <sup>-5</sup>
J214	GCAWPTYWNCG	1.4*10-6
J215	NCAWPTYWNCG	9.0*10-6
	<del></del>	

Figure 8 (Con't)



J216	VCAWPTYWNCG	2.8*10-6
J227	SFYEAIHQLLGV-NH2	6.4*10-6
J228	HPPLEHLKAFLL-NH2	2.4*10-5
J229	APTFYAWFNQQT-NH2	2.4*10 <sup>-6</sup>
S122	HPTSKEIYAKLLK	9.3*10-6
S123	HPSTNQMLMKLFK	1.6*10-5
S124	HPPLSELKLFLIKK	2.3*10-5

Clone	Sequence
H5 Parental	LCQSLGVTYPGWLAGWCA
H5-3-JBA5-IGFR	LCOSWGVRIGWLÄĞLCP
H5-3-E1A11-IGFR	VCQSLGITDLGLCAGWGA
H5-3-E4B10-IGFR	LCOSLGLTHPGFEAWLCA
H5-3-E4C10-IGFR	LCONFGVTDPGCFYGWFA
H5-3-JBB6-IGFR	PCQRLGDTHLCWLAGWFA
H5-3-E4A9-IGFR	LCOSSGLSFLGCLGWWA
H5-3-E2A12-IGFR	LCOSLGFTDLDWLACWFE
H5-3-E4A12-IGFR	VCQGLGVECPGWFAGWWA
H5-3-E1F9-IGFR	PCOSLGLTCSGWFEGWGA
H5-3-E4F11-IGFR	LCOGWGIRIGWLVGRCM
H5-3-E4A11-IGFR	LWOSVGIKYPGGLAGWLA
H5-3-E4G7-IGFR	QWQSLGVTCPGSWAELCA
H5-3-E1B9-IGFR	LCQSLGVTYWEGLAWLCA

20.0	26.2	31.0	28.4	18.6	27.9	27.2	27.7	40.2	24.3	29.7	21.3	31.9	1	E-Tag	Ratios ov
2.1	2.2	3.0	ພ . ພ	3. <b>5</b>	3.9	4.2	4.3	5.4	6.1	7.8	8.Q	16.3	1.2	IÇFsR	Ratios over Background
	;	:	;	;	:	;	:	1	<b>1</b>	•	!	•	:	Ħ	pnyc
1	•		;	;	:	:	;	ı F	;	1.	:	!	;	IGFR/IR	Compa
;	;	:	:	:	:	!	•	:	!	!	:	:	:	IR/IGFR	risons

	Sequence
JBA5 Parental	LCQSWGVRIGWLAGLCP
JBA5-4-2C12-IGFŖ	LCOSWGVRIGWLAGLCP
JBA5-2-1F9-IGFR	LCESWGVRIGWLAGLCP
JBA5-2-1E10-IGFR	LCOSWGVRIGWLVGLCP
JBA5-4-2A11-IGFR	LCOGWGVRIGWLAGLCP
JBA5-3-2A3-IGFR	LCQSWGVRIGWLVGLCP
JBA5-4-2A9-IGFR	LCOSWGVRIGWLTGLCP
JBA5-1-1B6-IGFR	MCQSWDVRIGRLGGQCP
JBA5-4-2B9-IGFR	LCQGWDVRIGQLAGLCP
JBA5-1-1H7-IGFR	LCQGWGVRIGWLAGLCP
JBA5-3-2C3-IGFR	LCOSWDVRIGWVAGLCP
JBA5-1-1G7-IGFR	LCQSWDARIGWLAGLCP
JBA5-2-1E9-IGFR	LCLG*DVRIGLLAGLCP
JBA5-2-1D12-IGFR	L*KSWDVRSGLMAGLCP
-	

42.2	39.4	26.2	35.5	24.9	39.6	39.6	34.6	34.7	44.1	42.5	48.1	46.8	31.5	E-Tag	Ratios ov
2.2	4.5	14.8	15.3	22.6	22.3	31.4	33.1	33.3	40.2	39.5	39.5	41.5	20.6	ICFSR	er Backgro
1.0	1.0	1.5	1.1	1.2	1.0	1.0	1.0	1.0	1.2	1.1	1.0	1.0	1.0	₹	pund
2.2	4.5	9.9	13.9	18.8	22.3	31.4	33.1	33.3	33.5	35.9	39.5	41.5	20.6	<b>IGFR/IR</b>	Compa
	0.2		0.1	0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	<0.1	IR/ICFR	risons

Clone	Sequence	
Design	LCQSWGVRIGWLAGLCP	
JBA5-4-G12-IR	LCOSWDACIONLVGLSP	
JBA5-4-G3-IR	LCRSWEECIGWLVGPQP	
JBA5-4-Ģ1-IR	LCQSWGECIDRLVGQGA	
JBA5-3-B1-IR	<b>LCOGWGVRIGWLAGLCP</b>	
JBA5-3-C1-IR	LCQGWAVHIGQLAGLCP	
JBA5-3-A6-IR	LCQGWGVHIGRLAGLCP	
JBA5-3-A2-IR	LCQSWGVRIGWLAGLCP	
JBA5-3-B7-IR	LCQSWGVHIGRLAGLCP	

Ratios over	er Backgrou	und	Compa	risons	
E-Tag	IÇFSR	₹	<b>IGFR/IR</b>	IR/IGFR	
:	:	:	:	:	
37.5	3.0	1.4	2.1	0.5	
4.5	2.5	1.1	2.3	0.4	
32.0	ယ် 2	1.3	2.5	Q . 4	
29.4	6.8	1.2	5.7	0.2	
36.3	7.5	1.1	6.8	0.1	
28.0	7.4	0.7	10.6		
10.2	4.8	0.4	12.0.	0.1	
39.2	15.2	1.2	12.7		

Ratios over Background E-Tag IGFsR IR

Comparisons
IGFR/IR IR/IGFR

37.8

Figure 10A

20F-4-D11-IGFR 20F-4-G4-IGFR 20F-4-G12-IGFR		20F-4-B3-IGFR 20F-4-B12-IGFR			<del>zi</del>	Clone Design 20F-4-B7-IGFR
VNYEMDKVPPMPWGGYWWLS MGGGLWVGVHIWPGYSWLSQ SDVWAQPQRRNDWPGYHWLS	WQQANLSNGGGRWGGYDWLM FGRGYGGDGGGYWSGYEWLA	PGKVKSGREWPGYGWLER.A	RPHRINPQDDAVWPGYLWLG HRGTVTGVWVARWPGYEWLS	HRGTVTGVWVARWPGYEWLS SDVWAQPQRRNDWPGYHWLS	HRGTVTGVWVARWPGYEWLS SDVWAOPORRNDWPGYHWLS	Sequence XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

3.2	3.9	5.0	5.1	6.6	10.1	17.3	9.8	17.6	7.2	13.7	13.9	9.7	8.9	10.9	•	E-Tag	•
. 0.9	0.9	1.0	1.3	2.7	9.9	14.4	2.4	16.2	2.5	3.9	10.1	4.7	4.7	3.7	1	IGFsR	
0.6	0.5	0.5	0.5	0.7	2.4	3.6	0.6	ა . 5	0.5	0.8	1.8	0.8	0.7	0.5	1	IR	
1.5	1.8	2.3	2.7	4.0	4.0	4.0	4.1	4.6	4.7	5.1	5.6	6.0	6.3	7.3	:	IGFR/IR	•
0.7	0.6	0.4	0.4	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.1	•	IR/IGFR	:

lone	Şequence
esign	xxxxxxxxxxxxxxxx
20β-4-A4-IR	WPGYLFFEEALQDWRGSTED
20β-4-F2-IR	SMFVAGSDRWPGYGVLADWL
.20β-4-E8-IR	VRGFQGGTVWPGYEWLRNAA

20F-4-C10-IR	20F-4-H10-IR	Design	Clone
IHSSDGIGAWGGYAWFRDVA	LDLASGDSWLGYDVLRGWLS	XXXXXXXXXXXXXXXXXXX	Sequence

10.2 3.1 2.4 1.3
3.1 2.4

Clone	Sequence
Design	XXXXXXXXXXXXXXXXX
R20 }-4-D10-IR	LGPLLRWGSEVCGVWPDLCE
R20 }-4-D9b-IR	PFGFGGRWWGI PRMWWYRNS
R20 }-4-H4-IR	<b>WWWGGRNRWWLERWGLGGER</b>
R20 1-4-A2-IR	GRVALWGPVWPRWWFMSRPV

Ratios ove	er Backgro	μnd	Comparisons	risons
E-Tag	E-Tag IGFSR III	₹	IGFR/IR IR/IGFR	IR/IGFR
;	:	1	1	;
21.5	1.0	8.0	0.1	8.0
32.6	6.8	15.1	0.5	2.2
11.6	1.7	3.6	0.5	2.1
	, ,	n J	ر د	ა _

R40-4-40F10-IR	R40-3-40A2-IR	Clone Design	
GRTSMAFVPPRHLQPELAPRPVRNHAWLVGGG	RGTRTDRLWKSGGFAIVPRWPCFSYHCLVEWITKTGSPG	Sequence XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	

	*		
44.6	•	E-Tag	Ratios ov
1.5	:	<b>IÇFsR</b>	Ratios over Background
2.7		F	
0.6	;	IGFR/IR IR/IGFR	Comparisons
1.8	1	IR/IGFR	risons

Clone	Sequence
Design	XXXXXXXXXXXXXXXXXX
R20-4-F10-IGFR	CLGAGSFRAGILCLGGLPVS
R20-4-F7-IGFR	GFWATACGGLQICEELGLKP
R20-4-H9-IGFR	<b>PLFCAYMAQALGLGQDLSCG</b>
R20-3-A4-IGFR	RHLLLPQIWIAS * GGWGMG

Ratios ov	E-Tag	;	35.5	29.1	25.7	15.6
Ratios over Background	<b>IÇFSR</b>	•	6.0	4.7	3.0	2.7
ņaņ	₹		;	. 1	1	;
Comparisons	IGFR/IR IR/IGFI	•	1		:	i t
risons	IR/IGFR	1	1	;	1	•

Clone	Sequence
Design	XXXXCXXXXXXXXXXXXXXXXXXXX
20C-3-H3-IGFR	<b>PHRLCGTDEYLMQDLFVRGLCRLIW</b>
20C-3-F4-IGFR	GLLFCKQLFTLAGLQPEAGCVSSSR
20C-4-C10-IGFR	IWIACLDELLRGQVWSSCRRRAPIG
20C-3-G5-IGFR	DWLRCLGVILSGGLTELANTGCVQG
20C-3-A2-IGFR	WFSFCLGGLLQAQEWSVWGRDVGCI
20C-3-B4-IGFR	GYSWLRDVLMEKQAQLKREGSVGRQ
20C-3-C6-IGFR	FLTRLLERLGLS*ERGEAGGPYAQA
20C-3-E2-IGFR	FSGFCMGLERLSQVSLGYCGAGQGG
20C-3-A3-IGFR	ISFRCQLFVLAGMHPCPVDVGGEGF
20C-3-B1-IGFR	NTPNCSQDWGQESGFMALLLALTCK
20C-3-F5-IGFR	LQGFCELLATVTGVTGLGCLDYQPI
20C-4-A7-IGFR	GSSICNLLARAQIVELALCEMGVQE
20C-4-F8-IGFR	LSFACLLSQLSGVVLPDCLLGED
20C-4-G11-IGFR	GEHFCQLLMSLCGDDCGPVNCGGGS
20C-3-E1-IGFR	GWFECLLASLVLQVPQGRSRASAVC
20C-3-B6-IGFR	YRQECACSVGAVGFLCGLACLARSG

37.3	34.0	24.7	30.5	33.3	35.5	30.2	33.7	34.8	34.8	39.8	33.9	29.3	35.5	34.4	28.5	;	Ratios ov E-Tag
32.8	5.1	.13.3	27.7	19.3	31.9	9.8	14.3	28.1	20.9	29.1	18.3	21.1	24.4	27.5	26.6	:	er Backgro IGFsR
13.7	1.6	2.8	5.3	2.8	3.9	0.9	1.2	2.0	1.4	1.9	1.1	1.1	1.3	1.2	1.0	•	IR IR
2.4	ن 1	4.7	5.2	6.9	8.2	11.2	12.4	14.2	14.9	15.2	16.9	18.7	19.2	23.1	26.6	:	Compai IGFR/IR
•	0.3					0.1			0.1	0.1	0.1	0.1	0.1	<0.1	<0.1	;	isons IR/IGFR

40r-4-C4-16rK	40F-3-A3-IGFR	40F-4-D10-IGFR	40F-4-B1-IGFR	40F-4-D1-IGFR	Design	Clone	
<u>EAPPAVGLOCEARE VRAVAHODOGOMGQDAV. AMOGIMADO</u>	LSCLAYSRHGIWRPSTDLGLGRSVGEGSVSTRWRGYDWFE	W. GYAWLS	GLDHSDAVGVHLGFAWPA. ARGRWEAGGLEDTWAGYDWL	<b>LSCLAYSRHGIWRPSTDLGLGRSVGEGSVSTRWRGYDWF</b>	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	Sequence	

	Ratios ov	er Backgro	und	Comparisons	SONS	
	E-Tag	E-Tag IGFsR IR	₹	IGFIVIR IR/IÇFR	RJĢFR	
•	1	;	:	!		
τ•,	4.9	4.6	0.3	13.1	0.1	
	4.1	3.0	0.2	13.1	Q.1	
	4.9	4.5	0.4	11.7	Q.1	
1.,	2.6	2.0	0.3	7.9	0.1	
	٠ 8	2.0	0 5	4.1	0.2	

F815-4-A11-IGFR	F815-4-C12-IGFR	F815-3-D1-IGFR	F815-4-G11-IGFŔ	Parental/Design	Clone
HLSVLEELSWGASLFGQWAG	FQSLLEELVWGAPLFRYGTG	HRFVREGLLWGAYQFCYCSG	HFYVLVERLSGÅSLFGSGSA	HLCVLEELFWGASLFGYCSG	Sequence

Ratios ov	er Backgro	hud	Comparisons	risons	
E-T:2	<b>IÇPSR</b>			IIVIGER	
39.1	1.8		0.1	15.4	
34.6 7.9 1	7.9		7.9 0.1	0.1	
14.9	1.0		0.5	2.0	
35.2	1.0	0	0.5	2.0	
5.4	1.0		0.5	2.1	

Clone	Sequence	
Parental/Design	HLSVLEELSWGASLFGQWAG	
NNKH-4-A9-IR	NLCRLEELAWGASLFGQCAG	
NNKH - 4 - H4 - IR	APVSTĘĘLRWGALĻFGQWAG	t
NNKH-4-B3-IR	HLSVLEERWWRESLFGQWAG	
NNKH-4-E1-IR	HLSVLEERWWRAALFGQWAG	
NNKH-4-E7-IR	HLSILEEQWWRESLFGQWAG	•
NNKH-4-G3-IR	HMSVEELSWWASLFGKQAG	
NNKH-4-B6-IR	HLSELEERWWRATLFGQWAG	
NNKH-4-A10-IR	HLSVLEELWWRESLFGQWAG	
NNKH-4-A5-IR	HLSLLEEQWWRESLFGQWAG	
NNKH-4-F11-IR	HLSVLEERWWRETLFGQWAG	
NNKH-4-C9-IR	HLSVLEEQWWRESLFGQWAG	
NNKH-4-D12-IR	HLSVLEEQWW.ESLFGQWAG	
NNKH-4-D10-IR	HLSVLEELWWREALFGQWAG	
NNKH-4-E5-IR	HLSVLEERWWRATLFGEWAG	
ŅNKH-2-A6-IR	HL.VLEELLWGVSLFRQWAG	
NNKH-4-F6-IR	HLSALEEQWWRATLFGQWAG	
NNKH-4-C7-IR	HLSVLEERWWRATLLESGQ	
NNKH-4-F7-IR	HUSALEELWWRETLFGQWAG	
NNKH-4-F8-IR	HLSVLEELWWRESLFGKWAG	
NNKH-4-E9-IR	HLSVLEEAWWRESLFGHWAG	
NNKH-4-E6-IR	HMSEQEELWWRATLFGQWAG	
NNKH-4-B7-IR	HLSVLEERWWRETLFGEWAG	
NNKH-2-83-IR	HRSVLKQLSWGASLFGQWAG	

.5 5.3	.5 12.9	18.2 3.8 2	.5 7.9	.6 11.0	.1 7.5	.7 1.4	.1 2.8	.4 1.4	.5 1.4	.6 1.2	.0 1.4	.3 2.3	.0 3.1	.6 4.6	.4 2.0	.2 1.3	.3 1.3	.9 1.3	.9 4.8	.6 2.8	.6 1.0	.3 1.0	.4 1.0	Ratios over Background E-Tag IGFsR IR	
. 7	.2	. 7		6		.4	. 9	5	6	5	. 7	. 9	.9	.9	N	-	ω	w	5	. 7		. 7	<u>,</u>		
7.4	1.7	1.4	1.3	<u>س</u> . ب	1.1	1.0	1.0	1.0	0.9	0.8	0.8	0.8	0.8	0.7	0.6	0.6	0.6	0.6	0.5	0.4	0.4	0.4	0.5	Comparis	
0.1	0.6	0.7	0.8	0.8	0.9	1.0	•	1.1				1.3	1.3	1.5	1.6	1.7	1.7	1.8	2.0	•		2.6	2.1	ons VICFR	

Clone	Sequence
Parental/Design	HLSVLEELSWGASLFGQWAG
NNKH-2-C5-IGFR	HL*VLEELSWGASLVGQWAV
NNKH-2-D9-IGFR	HLSVLEEL*LGASMFGLWAG
NNKH-2-H12-IGFR	HLSVLKELSW*ASLFGQWAG
NNKH-2-D10-IGFR	HLSALEELSWGASLFGQWAG
NNKH-2-G9-IGFR	HLSVLAELS*GALLFGQWAG
NNKH-2-C6-IGFR	RLSVLEQLSWGASLFGPWAG
NNKH-2-C7-IGFR	HL*VLVQPSWGASLFGQWAG
NNKH-2-F11-IGFR	HQSVLEELSR*ASLFGQWAG
NNKH-2-H3-IGFR	DMSVLGGLSWGA*LFGQWSG
NNKH-2-B8-IGFR	HLSVREGQLWRASMFGRWAG
NNKH-2-B12-IGFR	QLSVLVEL*WGASLFGPWAA
NNKH-2-F9-IGFR	HLSVGEELSW*VALLGQWAR

3.7	1.2	17.5	4.7	6.7	21.8	18.2	1.9	4.8	5.0	4.1	7.3	5.4	€-Tag	Ratios ov
0.6	1.0	3.7	0.7	1.3	1.3	1.0	1.4	2.1	1.3	0.5	0.9	1.0	IGESI	er Backgro
2.1	2.9	5.2	0.8	1.4	1.3	0.9	1.3	1.9	1.1	0.4	0.7	2.1	₹	ùnự
0.3	0.3	0.7	0.9	0.9	1.0	1.1	1.1	1.1	1.2	1.3	1.3	0.5	GFIVIR	Compa
w	2.9	سر									Q.8		INICER	risons



Antagonist	DD	Clonal Name 2013  2013  188 E7 188 20F1 40GF1 3GF1 20H1 20H1 10FR C1 A654-C1 10FR 112 A654-H2 10FR D5
1 1.1 YES Antagonist 9.7 1 1.1 YES Antagonist 9.7 1 2.3 Antagonist 9.7 1 3.6 Antagonist 19 1 0.84 Antagonist 12 1 0.62 Antagonist 12 1 0.62 Antagonist 12 1 0.49 Neutral 0.05* 1.12 Neutral 0.02* 1.14 Antagonist 5.4 1.15 Neutral 0.02* 1.12 Neutral 0.02* 1.14 Antagonist 5.4 1.15 YES -20 μΜ Agonist 5.1 1.16 Neutral 0.02* 1.17 Antagonist 5.1 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1		3 3 mre
1.1   YES   Antagonist   9.7     1   2.3   Antagonist   19     1   3.6   Antagonist   19     1   0.84   Antagonist   12     1   0.62   Antagonist   1.4     1   0.62   Antagonist   1.4     1   0.49   Neutral   0.05*     1   0.19   Neutral   0.02*     1   0.75   -20 μΜ   Agonist   5.4     1   0.70   YES   -20 μΜ   Agonist   5.1     1   0.70   YES   -20 μΜ   Agonist   5.1     2   0.25   YES   -20 μΜ   Agonist   1.3     2   0.25   YES   -20 μΜ   Antagonist   2.5     1   0   0.37   Antagonist   2.2     1   0.04*   Antagonist   5.20     2   0.25   YES   Antagonist   5.20     3   0.09*   Antagonist   5.20     4   0.09*   Antagonist   5.20     5   1   Antagonist   5.20     6   0.55   Antagonist   5.20     7   0.09*   Antagonist   5.20     8   2   2.20     8   2   2.20     8   2   2.20     8   2   2.20     8   2   2.20	8 ≡	
1   2.3   Antagonist   19     1   0.84   Antagonist   12     1   0.62   Antagonist   12     1   0.62   Antagonist   1.4     1   0.62   Antagonist   1.4     1   0.75   -20 μΜ   Agonist   5.4     1   0.75   -20 μΜ   Agonist   5.4     1   0.75   -20 μΜ   Agonist   5.20     1   0.70   YES   -20 μΜ   Agonist   5.1     1   0.25   YES   -20 μΜ   Agonist   1.3     2   0.25   YES   -20 μΜ   Agonist   1.3     2   0.25   YES   -20 μΜ   Agonist   1.3     2   0.25   YES   -20 μΜ   Agonist   2.5     2   0.25   YES   -20 μΜ   Agonist   1.3     2   0.25   YES   -20 μΜ   Antagonist   2.2     3   10   1.1   Antagonist   -20     4   0.00*   Antagonist   -20     5   1   3   Antagonist   -20     6   0.55   Antagonist   -20     7   0.00*   -20     8   2   -20     8   2   -20     9   2   4   -20     10   1.3   Antagonist   -20     10   -2   -2     10   -2     10   -2   -2     10   -2     10   -2   -2     10   -2	1-1	40G11
20111   1   3 δ   Antagonist   12   10   1   0.84   Antagonist   12   10   0.84   Antagonist   12   10   0.62   Antagonist   1.4	~	3011
G3	9	20111
102	ē	GJ
IGFR C1	Ξ	D2
IGFR	7112	7654-C1
IGFR Λ6     1     8.1     Neutral     >20       IGFR D3     1     8.1     ×20     Neutral     >20       IGFR D3     1     8.1     ×20     ×20     ×20     ×20       IGFR II2C     1     0.70     YES     -20 μΜ     Agonist     6.1       20E2     2     0.25     YES     -20 μΜ     Agonist     1.3       20C11     2     0.25     YES     -20 μΜ     Agonist     1.3       E8     10     0.37     Antagonist     2.5       F2     10     1.1     Antagonist     2.2       20A4 (A7)     6     1.2     Antagonist     >20       D8     6     0.35     Antagonist     >20       F8     4     0.04*     Antagonist     >20       IGFR E4     1     2.6     ×20	Ē	A65-4-1+2
IGFR DS   1   8   20   20   20   20   20   20   20	Ī	IGFR A6
IGFR JBAS       9       4.4 cycli       >20 μΜ       Agonist       8.1         IGFR IJZC       1       0.70       YES       -20 μΜ       Agonist       6.1         20E2       2       0.25       YES       -20 μΜ       Agonist       1.3         20C11       2       0.25       YES       -20 μΜ       Agonist       1.3         E8       10       0.37       Antagonist       2.5         F2       10       1.1       Antagonist       7.4         20A4 (A7)       6       1.2       Antagonist       >20         D8       6       0.55       Antagonist       >20         F8       4       0.04*       Antagonist       >20         IGFR E4       1       2.6       >26       >20	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	IGFR DS
1   20E2   2   0.25   YES   -20 μM   Agonist   5.1   5.1   20C11   2   0.25   YES   -20 μM   Agonist   1.3   1.3   20C11   2   0.25   YES   -20 μM   Agonist   1.3   1.3   2.5   2.5   20A4 (A7)   6   1.2   Antagonist   2.2   20A4 (A7)   6   1.2   Antagonist   2.2   2.		IGFR JBAS
20E2       2       0.25       YES       ~20 μΜ       Agonist       1.3         20C11       2       0.25       YES       ~20 μΜ       Agonist       1.3         E8       10       0.37       Antagonist       2.5         F2       10       1.1       Antagonist       7.4         20A4 (A7)       6       1.2       Antagonist       >20         D8       6       0.55       Antagonist       16         F8       4       0.04*       Antagonist       8.2         IGFR E4       1       2.6       2.5		IGFR 112C
20C11 2 0.25 YES -20 μM Agonist 13  E8 10 0.37 Antagonist 2.5  F2 10 1.1 Antagonist 7.4  20A4 (A7) 6 1.2 Antagonist >20  D8 6 0.55 Antagonist >20  F8 4 0.04* S20  IGFR E4 1 2.6 >20  I		20E2
E8 10 0.37 Antagonist 2.2  F2 10 1.1 Antagonist 7.4  20A4 (A7) 6 1.2 Antagonist >20  D8 6 0.55 Antagonist >20  F8 4 0.04* 8.2  IGEN 756 1 2.6 >20    Compare 10		20011
F2     IV     1.1     Antagonist     7.4       20A4 (A7)     6     1.2     Antagonist     >20       D8     6     0.55     Antagonist     16       F8     4     0.04*     >20       IGFR E4     1     2.6     >20	2 2 2	EX
D8 6 0.35 Antagonist >20  F8 4 0.04* 82  IGFR E4 1 2.6 >20  Antagonist   16  8.2  >20  >20    13   20    20		F2
F8 4 0.04°	7710	20A4 (A7)
F8 4 0.04° 8.2 1GFR E4 1 2.6 >20 1GFR E4 1 2.6 >20		D8
1GFR 530   2.6   >20	-	**
		ICEN DA



•				120	NOW: BACTOR WITHOUT COLOR	96	S176	\$17%
	‡	0.9 nM	2-4 ILM	230 nM	GRVDWI.QRNANFYDWFVAELG	A6	S175	S175
				Mul 91	PLAELWAYFEIISEQGRSSAII	RI36	S174	S174
				1.2 jtM	LDALDRIMRYFEERPSL	RB6	S173	S173
	•		No Binding	>20 JuM	AFYDWI:AKK	8	S167	\$167
					WPGYLFFEEALQDWRGSTED	GROUP 6		RP-24
					GSASFYDAIDŘLLŘMŘÍKK	136		RP-20
					LKDGFYDYFWQRLHLGSKK	A6		RP-19
1					LQPCSGFYECIERLIGVKK	136		RP-18
			M™ 01<		QSDAI:YSGLWALIGLSDGKK	В6		₹-17
					V,DARDD[FUJL;SE;VTLL	B6		KP-16
					SQAGSAFYAWFDQVLRTVKK	A6		RP-15
١			Mrt 01<		SACQFIXCHENFYDWFARQKK	A6		2-14
			×10 ¼M		ASGFPENFYDWFGRQLSLKK	۸6		ΑP-13
					DPFYQGLWEWLRESGKK	86		KP-12
	+		Mri 01<		QAPSNFYDWFVREWDKK	8		Α'-11
	+		M <sup>2</sup> √01<		GSFYEALQRLVGGEQGKK	136		KP-10
	‡	2.9 nM			GSLDESFYDWFERQLGKK	>6		2
				÷	QSFYDYIEELLGGEWEE	136	7878	KT-88
	+		>Տ յվM		QSFYDYIEELLGGEWKK	136		K7-8
					AAVIII:QFYI)WFADQYKK	>6		2.7
	#		4		TFYSCLASLLTGTPQPNRGPWERCRKK-Biotin	C-C		10°-8
	•		<b>آس</b> ر 6		AGVNAGFYRYFSTLI.DWWDQGKK-Biotin	136		25.5
-	+		Wil S		PPWGARFYDAII:QLVFDNL	136		Ž
	:		×۱ö سل		GRFYGWFQDAIDQLMPWGFD	\$		E.S.
	+		۲ <u>۰</u> ۳		RSEASFILVEFYSWFEEQLRS	76		RP-2
	+		, Wri I		GSRPVFHEQFYEWFVDQLGL	\$		<u> </u>
	•		* *		RAMSFYDALVSVLGLGPKK-Biotin	106	-	NG-G9
			کا ای <u>لا</u> الکام		VEGRĞLEYDLLRQLLARRQNG	D6		NG-G8
	‡	4.2 nM	2-4 JuM		GIISQSCPESFYDWFAGQVSDPWWCW	8		NG-G33
1					GNGIXGMFYQI.LSI.LVGRDMH	136		NG-C2
			uni  >		FYCGLEELSWGAALFGYCSG	136		KCG7
					GLEQGCPWVGLEVQCRGCPS	C-C-C		KC-G2
					RLYYEWFWGQLEAQGRGGLS			KCF9
‡	‡	S nM	ντι ς<	700 n.M	FIII:NFYDWFVRÓQVSKK	A6	D117	112C
				40 nM	KIII.CVLELEWGASLEGÝĆŠGKK	CCLOOP	12124	×
				370 nM	KRGFQGGTVWPGYEWLKNA	GROUP 6	D120	8
	0			Mn 055	KWI.DQI:WAWVQCI:VYGRGCPSKK	C-C LOOP	10123	108
	-			490 nM	DYKIX WARPCGDAANF YDWF VQQAS KK-biotin	λ6	13112	CI
+	+	2.8 nM	, a	250 nM	DYKDFYDAIDQLVRGSARAGGTRDK K-biotin	=		7:1:07
1	֡							
Assay		S175	Blacore		Deglence	2000	2 In a C	SHIEN

Figure 11B



Clonal	Dor S.			IR-Kd	IR.IC.	IR.IC. ED.	3	Feb (2)
Z me	name '	Moilf	Sequence		Blacore	S175		
S177	177	136	EIIWNT VDFFYFTLFEWLRESG	77,M	21111			
\$178	S178	16	FILWNI VIDELAU ALEGE	130				
0110	3			1701001				_
31/9	21/9	20	QSDSGT VIIDRFYGWFRDTWAS	540 nM				*
F8-C12	S224	C.C 1.00P	FQSLLEHLVWGAPLFRYGTG					
S225	S225	CC1.00P	PI.CVI.EELFWGASLFGYCSG					
128.61	S226	C-C LOOP	QLEEEWAGVOCEVYGRECPS					
S264	S264	۸6	IQGWEPFYGWFDDVVAOMFEE					
S257	\$257	116	RWPNFYGYFI:SI.I.TIIFS					
S258	S258	136	HYNAFYEYFOVI.LAETW					
S2'59	\$259	116	EGWDFYSYFSGLLASVT					
•	•							

Figure 11B (Con't)



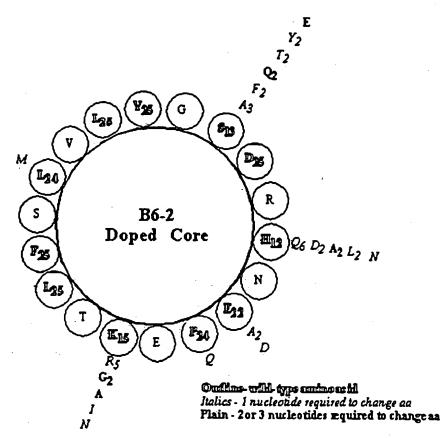


FIGURE 12



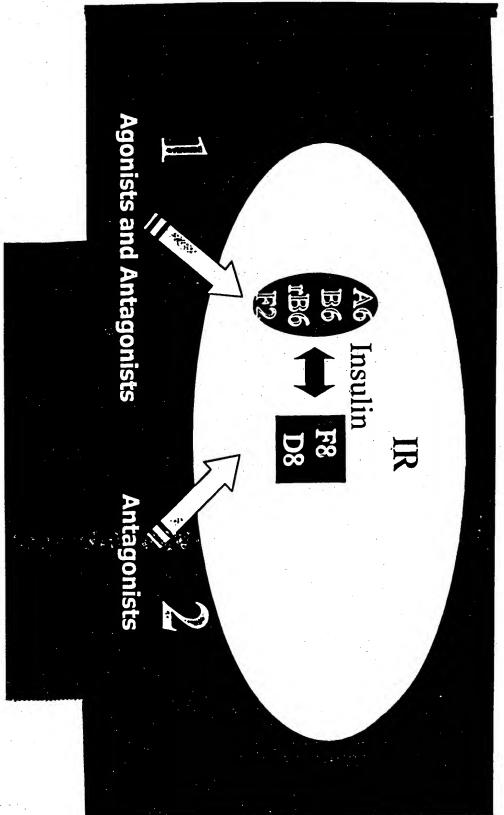


FIGURE 13



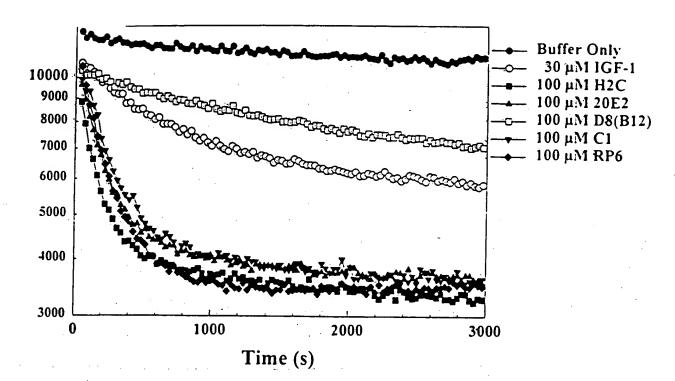
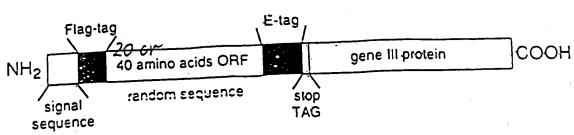


FIGURE 14

Site 2 Binding Intra-receptor Binding to IR **Di-Peptides** nter-receptor FIGURE 15 上度 PA 民國

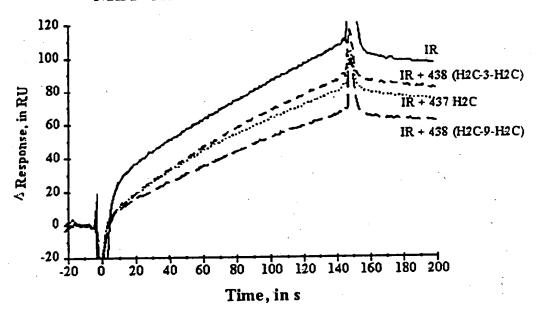








MBP-H2C homodimer s



Class II clones  D5 DYKDPLYGGGIHLYYPGTMGYVPGFPRQVKVLGDADKNFYDWFM  A6 DYKDYRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDWFV  R35 DYKDSGCCRLLGLRWMFIVIVGWSGALVCQSAASAAGFYDWFV	Class I frameshifting clones (all in +1 frame)  F6 2x TTKTRG.IFGMLLGVLREQILLWPFPKDCVQMKDIFYSLLASL  7 3x TTKTRIGCCS.LVWGWRGCRLADGFYAFLMALAG  B TTKTRIGKFAWVLAFSVQGVGVAFYSALAALLCAHSASLVCG	human IGF mature VCGDRGFYFNKPTGYGSSSR human IGF propeptide MSSSHLFYLALCLITFTSSA	Class I clones  16 3x DYKDAETPAQVGWNRLWSVWPGEHWNTVDPFYHKLSELLRESGA E5 2x DYKDRGGMDRQWLDVGARHRLERRSVQDNTDDFYGGLRILVDGF 9 DYKDGPPDSFDVTEKGDMAILNVRFDPHSLDFNDQTFYFLLDSL G6 DYKDGPPDSFDVTEKGDMAILNVRFDPHSLDFNDQTFYFLLDSL 12 DYKDAPLDARLSAPRFQWSPRTWRQSLSYGEWSCGSFYDCLSSI A5 DYKDMGSSQFQDTRPSSGQAYSHSLDSDGWGTANWIFLRALEGL C6 DYKDSGAAHEGNQGRERSTHLAANINDHLPGDAGIWLGYSWLS Consensus (regular+frameshifters) d.fy.llsal
<b></b>	1 1 3 /CGA 1		# Clones: Rnd 3 Rnd 4 1 2 2 2 1 1 1 1 1 1 1
nd	nd +		Compet- ition  +  +  nd  nd  nd  nd  nd  nd  nd  nd

human IGF mature (1-70)

GPETLCGAEL VDALQFVCGD RGFYFNKPTG YGSSSRRAPQ TGIVDECCFR SCDLRRLEMY CAPLKPAKSA

nd = no data



FIGURE 18

FIGURE 19

CONTRING ATTROCTION COUTTING COTTITION COCCCIOCCI COCCCOCCO CA 112

IQF-05 באכזאנאאה אכופכחופר חפכחופפר פובאובאחא פנדודורופ ודואפניפפר נפפופופנר ודדואנונאס נפחפננופנ נחפרופום פני CACIACAMO ACCICUIRCE COCICCIETI COICEMEGO COICAIGACE CITITIATOS COTICICOS AIGCIGANOS CICCIGGAIC ICCOCCOCA 1880

gtgtggtgcg gcggccgca 139

CACIACAMO ACTICOGOTI CANTITICO INICITACIO COCCIOCITA COTTICACAT ICTICITOS COCTITICIA ACCATIGISI ICAGAIGAMA GAIATTITTI ATTICATION COCTACTING CCCCCCCCA

13

içr.s

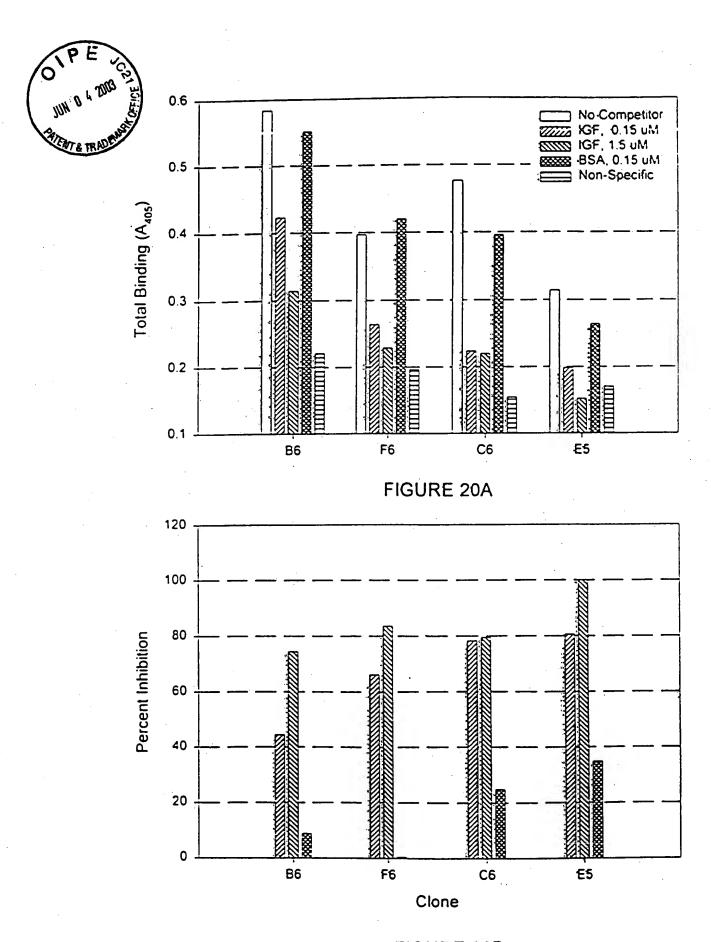
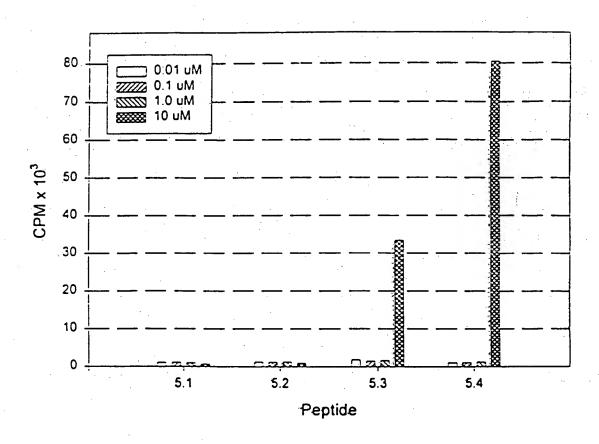


FIGURE 20B







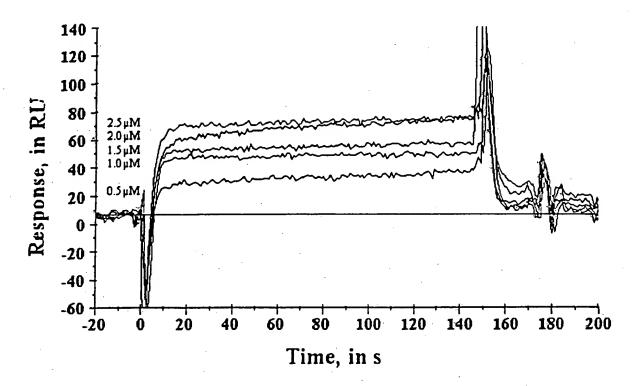
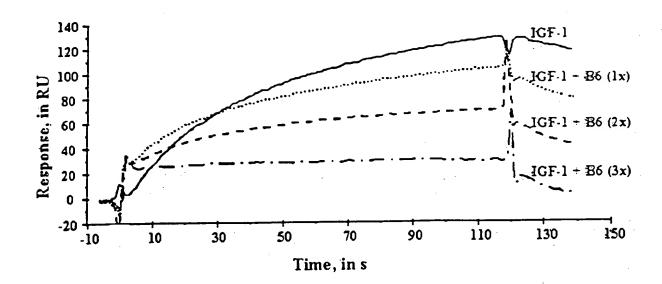


FIGURE 24A







GACTACAAAGACGACGATGACAAGTACCGTGGTATGCTGGGTCGTATCTCTGACG
D Y K D D D D K Y R G M L V L G R I S D

GTGCTGGTAAAGTTGCTTCTGAACCGCCGGCTCGTATCGGTCAGAAAGTTTTCGCTGTTAA
G A G K V A S E P P A R I G Q K V F A V N

CTTCTACGACTGGTTCGTTGCGGCCGCA 96 nt
F Y D W F V A A A A FIGURE 25A

CTACAAAGACGACGATGACAAGTACCGTGGTATGCTGGGTCGTATCTCTGACGGTGCT GGTAAAGTTGCTTCTGAACCGCCGGCTCGTATCGGTCAGAAAGTTTTCGCTGTTAACTTCTACG ACTGGTTCGTTGCGGCCGCAGTGTGA 154 nt

FIGURE 25B



TTNNKNNKNNKNNK V X X X X 21 aa

FIGURE 26A

CTACAAAGACNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKAACTTCTACGACTGGTTCGTTNNK NNKNNKNKGCGGCCGCAGTGTGA

FIGURE 26B



HS .	NH:-D-Y-K-D-L-C-Q-S-L-G-V-T-Y-P-G-W-L-A-G-W-C-A-K-K(Bictin)-COOH
HS Control	NH2-D-Y-K-D-W-C-L-T-L-Q-F-L-V-W-A-3-G-G-G-Y-C-A-K-K(Biotin)-CCOH NH2-D-Y-K-D-V-C-Q-R-L-G-G-T-F-P-G-W-L-V-G-V-C-R-K-K(Biotin)-CCOH
	NH2-D-Y-K-D-L-C-Q-R-L-G-V-G-W-P-G-W-L-S-G-W-C-A-K-K(Bictin) -COOH
H5-447 H5-432	NH <sub>2</sub> -D-Y-K-D-L-C-Q-S-L-G-V-T-W-P-G-W-L-A-G-W-C-A-K-K(Biotin)-COOH

## FIGURE 27



Clone:			:Bindin	g Ratios:	
Cione.			Target	€∙Tag	% Max
			7	27	26
A6S-1-C5	DYKD	RIHNOTERSGNFYDWFVHQLV AAA VATVHVGGGMNFYDWFVAQVG AAA	7	_	26
A6S-1-G3	DYKD		5	19	
A6S-1-A2	DYKD	KDPVTVSQGRNFYDWFVVQIQ AAA	5	-20	25
A6S-1-D5	DYKD	RVGSGMEDLGNFYDWFVRQAQ AAA	5	25	20
A6S-1-H4	DÄKD	HKSWTTMSPLNFYDWFVAQVE AAA	3	18	17
		·			
AEC 2 E2	DYKD	LAMSVASRPANFYDWFVAqIV AAA	30	35	86
A6S-2-F2 A6S-2-D2	DYKD	RAERGSMRDSNFYDWFVQQLP AAA	30	36	83
A6S-2-E3	DYKD	VqEGLSGMEGNFYDWFVDQLF AAA	28	36	78
	DYKD	RGGRESDSGTNFYDWFVGAIR AAA	28	40	70
A6S-2-H2		SRAPYGSTAGNFYDWFVQAVS AAA	25	37	68
A6S-2-A3	DYKD	RVGIqVDPHTNFYDWFVIQLT AAA	27	42	64
A6S-2-H1	מאוט	RVG1qVDFh1Ht4DHt41QBt AAA	٠,		•
A6S-2-F1	DYKD	VGqVGRYVRSNFYDWFVQqAM AAA	8	30	27
A6S-2-G1	DYKD	RPqLVESGSKNFYDWFVqVVR AAA	8	30	27
A6S-2-B2	DYKD	EMYGDTSERVNFYDWFVSALq AAA	. 5	30	17
A6S-2-A1	DYKD	LSSRGRVTMRNFYDWFVAqVV AAA	3	31	10
•					
		•			,
A6S-3-E1(	DYKD	RVREKLPRPENFYDWFVNqIH AAA	22	23	96
A6S-3-G2	DYKD	TWMWEERKODNFYDWFVGQLK AAA	20	21	95
A6S-3-E5	DYKD	RYRGERHDGRNFYDWFVEqVN AAA	19	21	90
A6S-3-H2	DYKD	qGAEGRLSEGNFYDWFVQAVS AAA	19	21	90
A6S-3-H9-	DYKD	YSIEVQDWNENFYDWFVSQLG AAA	20	- 23	87
A6S-3-G3	DYKD	PRLHMGSDMGDFYDWFVVqIA AAA	18	21	83
A6S-3-F8	DYKD	GRGGGLKRPDNFYDWFVAAAK AAA	-20	25	80
A6S-3-G1	DYKD	GAVGLAEAGPNFYDWFVSqVq AAA	19	24	79
A6S-3-H1	DYQD	PASNKNSLAENFYDWFVqQTR AAA	23	30	77
A6S-3-E6	DYKD D	ARDHGVWVMSNFYDWFVAqVS AAA	5	20	25
A6S-3-D9	DYKD	SLQGADFQQGNFYDWFVSELA AAA	4	17	24
A6S-3-E3	DYKD	RPSLPEVRPGNFYDWFVqSVR AAA	4	19	21
A6S-3-H8	DYKD	NPTSVqQYGVNFYDWFVNVLS AAA	- 4	-20	20
A6S-3-G4	DYKD	CADPGACSSLNFYDWFVqMRG AAA	4	21	19
A6S-3-B10	DYKD	YDqDPPYWGLNFYDWFVREVA AAA	3	16	19
A6S-3-C1	DYKD	RPVIGGGGTRNFYDWFVAqMI AAA	3	17	18
A6S-4-G5	DYKĐ	QEVTRTRDDKNFYDWFVSqIF AAA	26	18	144
A6S-4-D2	DYKĐ	PPYRSSRLGENFYDWFVMqVR AAA	26	19	143
A6S-4-F6	DYKD	LKGSSQPLSVNFYDWFVQQIK AAA	24	17	142
A6S-4-H4	DYKD	PRMVERPSEDNFYDWFVTqLS AAA	-28	20	141
A6S-4-C1	DYKĐ	CWARPCGDAANFYDWFVqQAS AAA	22	16	141
A6S-4-G3	DYKD	GAQAIREIHHNFYDWFVAQVT AAA	29	21	139
A6S-4-H3.	DYKĐ	GRGDQRHETTNFYDWFVRELq AAA	28	20	137



	VARU	GSIAQLIMRANFYDWFVEqTN	AAA	24	1-8	130
A6S-4-H5.		RLMGGIAEPQNFYDWFVREVA	AAA	25	20	126
A65-4-G6	DYKD	HHSPGNEHGYNFYDWFVLQVA	AAA	24	19	123
A6S-4-H5	DYKD	ERSAAGFREGNFYDWFVAQVN	AAA	32	27	120
A65-4-E4.	DYKD	GSQHSGREPHNFYDWFVAQVG	AAA	28	24	120
A6S-4-F5.	DYKD	GSUNSGREPHNEIDHIVAGO	AAA	21	18	118
A65-4-D4	DYKD	IARMRETFQPNFYDWFVDQLA	AAA	28	25	116
A6S-4-C6	DYKD	RLDRSSTSGVNFYDWFVAQVG	AAA	23	20	116
A6S-4-D3	DYKD	GLRSEQGNRLNFYDWFVAQIA	AAA	26	23	115
A6S-4-F2	DYKD	SVIQTRQDETNFYDWFV?AMS	AAA	22	19	115
A65-4-A5	DYKD	VEVORHIRKONFYDWFVKQID	AAA	24	21	114
A6S-4-C3	DYKD	VTMLDKGAQDNFYDWFVREVA		30	26	113
A6S-4-F3	DYKD	HNSSSPMRTGNFYDWFVQELR	AAA	•	19	113
A6S-4-B4	DYKD	ERSPRPALASNEYDWEVQQVV	AAA	21		113
A65-4-B6	DYKD	SDARQAGLQENFYDWFVSQVR	AAA	26	23	
A6S-4-B1	DYKD	RHERGKEGPGNFYDWFVSQVV	AAA	21	19	112
A6S-4-G4	DYKD	SALSGPVqPINFYDWFVTGM	AAA	30	26	112
A65-4-A6	DYKD	HVEHMAVGDGNFYDWFVVQLR	AAA	23	21	111
A6S-4-F4	DYKD	VGHSGVPPYPNFYDWFVMQVS	AAA	24	22	110
A6S-4-D6	DYKD	LGAAETWDGINFYDWFVKQVS	AAA	24	22	110
A6S-4-E6	DYKD	RSSGGLLSqGNFYDWFVSQLE	AAA	26	24	109
A6S-4-A3	DYKD	LAINDLVTHKNFYDWFVDQLR	AAA	2-0	18	109
A6S-4-E3	DYKD	RGMTGMVGRGNFYDWFVGQLR	AAA	23	21	109
A6S-4-A2	DYKD	IGGQGQHQDGNFYDWFVEALA	AAA	22	2-0	107
A6S-4-B2	DYKD	QSVDLSRPDSNFYDWFVEVLS	AAA	22	21	105
A6S-4-H2	DYKD	VTFTSAVFHENFYDWFVRQVS	AAA	20	19	104
A6S-4-D1	DYKD	SNPSRQDASVNFYDWFVREVA	AAA	22	22	103
A6S-4-H1	DYKD	IVAGARHSEVNFYDWFVIQVR	AAA	18	18	102
A6S-4-E2	DYKD	?DGQSVSSKGNFYDWFVQqMT	AAA	25	25	101
A6S-4-G1	DYKD	AELVGAGVRGNFYDWFVDQLV	AAA	16	16	101
A6S-4-G2	DHKD	SAGHHMPRESNEYDWFVDQVV	AAA	24	25	99
A65-4-A1	DYKD	DSSRLWLGERNFYDWFVAGIS	AAA	12	17	68



- - 1.2	-	2.6
10 ~17.5 1 16.4 5 -11.7 1 9.9 14 ~8.5 6 -8.3 1 8.3 1 6.0 1 5.8 3 5.5 3 2.7	~55 58	1.2 1.1 1.0 1.2 0.7 1.0 1.1 1.2 1.3 1.4 1.1
	- 1.1  19	- 1.1 - 19 -24.0 -45% 10 -17.5 -54 1 16.4 50 5 -11.7 -50 1 9.9 -51 14 -8.5 -65 6 -8.3 -65 6 8.3 68 1 6.0 50 1 5.8 67 3 5.5 60 3 -5.3 -55



## Genomic rvab Library

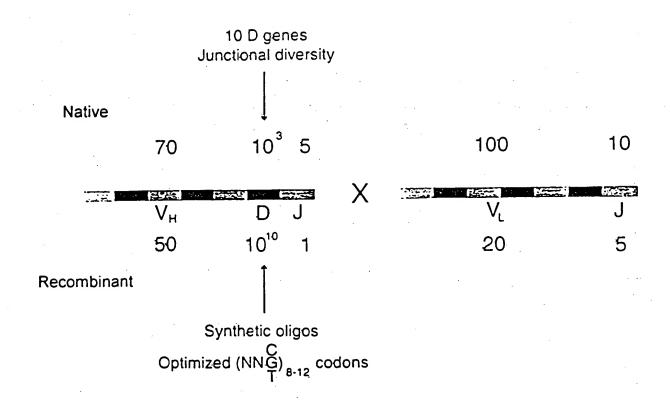


FIGURE 30



## VH Gene Sequences

DP-1 **DP-10 DP-12 DP-14 DP-15** DP-2 **DP-21 DP-25** DP-29 **DP-30 DP-31 DP-32** DP-33 **DP-35 DP-38** DP-39 DP-40 **DP-42** DP-44 **DP-45** DP-46 **DP-47** DP-5 DP-50 DP-51 DP-52 DP-53 DP-54 DP-59 DP-63 **DP-66 DP-67 DP-68** DP-69 DP-7 DP-70

DP-71 DP-73 DP-74 DP-8 hv1263 VHD26

## Lambda and Kappa Gene Sequences

DPK11 DPK15 DPK18 DPK2/L14+ DPK3/L11+ DPK4 DPK6 DPK8/Vd+ DPL23 HK101 L22+ L23/L23a LFVK431 VA++



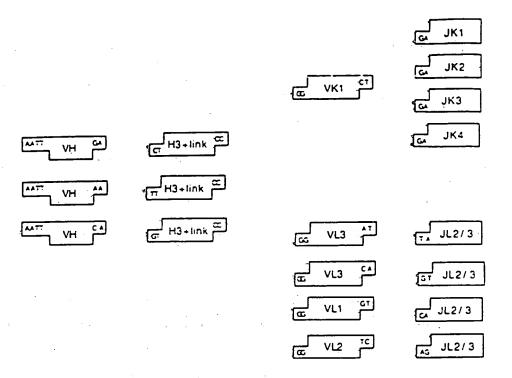


FIGURE 32



Lambda 2 gene:

GGNNN-----G

NNN-----CTC

GTG---

continued as for JL2/3

for DPL11

DPL11

GCNNN-----G All kappa genes: GGCCTTAAGCCGGGTCGGCCGGNNN----N CCGGAATTCGGCCCAGCCGGCCNNN-----NCA GCCTTAAGCCGGGTCGGCCGGNNH-----N CCGCAATTCGGCCCAGCCGGCCHHH · · · · · · · · IIAA GGCCTTAAGCCGGGTCGGGCCGGHHH-----H CCGGAATTCGGCCCAGCCGGCCHHH-----HGA Lambda 3 gene: Lambda 3 genes: Lambda 1 genes: (except VK L20) 426 NNN -----CCT J' and for 40 VII genes )' end for 4 VH genes: DP2, DP3, DP5 and DP38 )' end for 7 VH genes: DP31; DP33, DP39, GGNNN-----C GGNNN-----G GGNNN-----C C 1:3 / DPL2+DPL3 Ser Ser NNN-----CCA NNN-----CAT ć] r NNN------GGT /DPL23 (=VL3.1)/ DPL16 (=v3s1)+ GAAAGTGAAAGCCGGGACCCTGGTTTCACCTATAGTTT GAATGTGAAAACCGGTCCCCTGGTTCGACCTCTAGTTT **GAACCTGCAAGCCGGTTCCCTGGTTCCACCTTTAGTTTCGCCGGCGTCACACTCACGTTTTCTAQAGC** GAGAGTGAAAGCCGCCTCCCTGGTTCCACCTCTAGTTT 91CA+ /
PheThrPheGlyProGlyThrLysValAspileLys
TTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA continued as for JKl TrpThrPheGlyGliGlyThrLysValGlulleLys
TGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAAGCGGCCGCAGTGTGAGTCCAAAAAGATTTCG CTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA continued as for JKI LeuThr PheGlyGlyGlyThr LysValGlulleLys TACACTTTTGGCCAGGGGGACCAAGCTGGAGATCAAA TyrThrPheGlyGlnGlyThrLysLeuGlu1leLys VII gene EIIS CLY JK1 gene JK2 gene JK4 gene CTRNM - - - NUM CTHHV---HIVACCCCGGTCCCTTGGGACCAGTGGCAGAGGAGTCCACCTCCGCCAAGTCGCCTCCGCCTCCACCGAGACCGCCACCGCCTA WILL- - - WIELL / JL2/3 for DPL16+v3s1+v318 / Hot1 / PCR primer site / ValValPheGlyGlyGlyThrLysLeuThrValLeu GTGGTATTCGGCGGAGGAGGACCAAAGCTGACCGTCACAGCGGCGGCGGCAGTGTGAGAGCCAAAAAGATTTCG TACACCATAAGCCGCCTCCCTGGTTCGCAGGATCGCAGGATCACACTCAGGTTTTCTAAAGC CACAC---GTCAC--for DPL23+VL3.1 HIB---- HIBTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAATCC for DPL2.DPL3 NNK - - - NNK MAN --- MAN CTG---CTC--continued as for JL2/1 continued as for JL2/3 DP40, (lpl. DP47 and DP49 continued as for J4b gene and linker continued as for J4b gene and linker continued as for JKI Notl / PCR primer site BOLD . IN DC! COLLECTION G4S linker

FIGURE 33



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CCCACCCCC	CCATGGGGCA GGTGCAGCTG	GICGAGICIG	GGGGAGGCTT GGTAAAGGCT	60
0002.2000	QVQL	V E S G	G G L V K P	
CONTRACTO	TTAGACICTC CEGEGGAGGC	TCTGGALTCA	CTITCAGTAA CGCCTGGAIG	120
GGSL	R L S C A A	SGFT	FSN AWM	
				100
AGCTGGGTCC	GCCAGGCTCC AGGGAAGGGG	CTGGAGTGGG	TTGGCCGTAT TAAAAGCAAA	180
SWVR	QAPGKG	LEWV	GRIKSK	
				240
ACTGATGGTG	GGACAACAGA CTAGGCTGCA	CCCGTGAAAG	GCAGATTCAC CATCTCAAGA	240
TDGG	TTDYAA	PVKG	RFTISK	
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GATGATTCAA	AAAACACGCT GTATCIGCAA	العالم المحالم	TCAAAACCCA CGACACAGCC	300
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			COMPANY MEASURE	360
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TGGTTTCAGC	AGAGGECAGG CCAATCTCC	AGGEGECTAA	TTTATAAGGT TTCTAACCGG	600
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GACTICTICGGG	TCCCAGACAG ATTCAGGGG	AGIGGGICAG	GCACTGATTT CACACTGAAA	660
DSGV	PDRFSG	S G S G	TDFTLK	
ATCAGCAGGG	TGGAGGCTGA GGATGTTGGC	GITTATTACT	GCATGCAAGG TACACACTGG	720
ISRV	EAEDVG	VYYC	мостны	
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CCTTACACTT	TITEGECAGGG GACCÁAGCIK	CACATCAAAC	GGGGGGC	767
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V Y Y C T T P G W Y G A E D K W G Q G T	
CTCCTCACCG TCTCCTCACG TCCACCCGGT TCACCCGGAG GTCCCTCTGG CCGTCCCCGA	420
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SDIQ MTQ SPS SLSA SVG DRV	
	£40
ACCATCACTT GCCGGGGGAG TCAGGGGAIT AGCAATTATT TAGGCTGGTA TCAGCAGAAA	540
TITCRASQGISNYLAWY QQK	
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CCAGGGAAAG TTCCTAAGCT CCTGATCTAT GCTGCATCCA CTTTGCAATC AGGGTGCCA	-600
PGKV PKL LIY AAST LQS GV P	
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(		<u> </u>	C÷C	$\infty$	AGI	CI	CC	ATC	CIC		IGICI	G	IAIC -	NG.	فكتا	عنی ا	يتسكة	لماتنات	(m)	.وحمان ب	بالسمند	1	400	
(	Q	М	T	Q	2	5	P	S	·S	·L	S	A	S	V	G	ט	R	V	1.	÷	1			
																						_	<b>5</b> 4 0	
•	īĢ	333	X	12.A	GIC	140	$\mathfrak{S}$	CAT	TH	-	AIGAI	, T.		$\mathfrak{C}\mathfrak{R}$	<b>SI</b>	ATC	333	C	. AC		33	À	540	
(	С	R	Ä	S	(	2	G	I	R	N	Đ	L	G	<b>.</b> ,	Y	Q	Q	K	P	G	K			
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	GO	$\alpha$	-	æ	TC		<u>r</u>	CIA	TG	TG	CATCO	: 24	ETT.	TAC:		GIG	Œ	TCCC	TA C		<b>II</b>	C	600	
	2	P	K	L		2	I	Y	A	A	°S	S	L	Q	S	G	v	P	S	R	F			
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	20	بيك	~~2(	-111	(2)	<u> </u>	4	~2	. 200	بلبلة	TCACI	٠.٠	RCA(	CA.	TCA	GCA	Œ	TCC	4 63	CIG	AACA	$\mathbf{T}^{\circ}$	660	
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	_	<del>~~</del>	~~ ~ .	~~~	• • • • • • • • • • • • • • • • • • •	т.	40	*17*1		3.50	ATTAC	, A	ינים	مرم		. 432	بلبلت	حوبو	: 17:	تعت	رجحر	٠ د	720	
	T1 _	بريز	انتونس 	-11 1	بلظ	ندسيل م	-10	7 T	سنهم .	رد. درست	A Let Test	 "N	ה דדע	U UTC		, 1 <del>0</del> 7			c.			-	•	
	F	A	T	Y		Y	C	ı	Q	IJ	Y	Ŋ	Y	٦	ı	, 1	r	G		,	•			
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							<b>C</b> C	W.	Œ	_													745	
	Х	V	Ξ	Ι	i	K																		



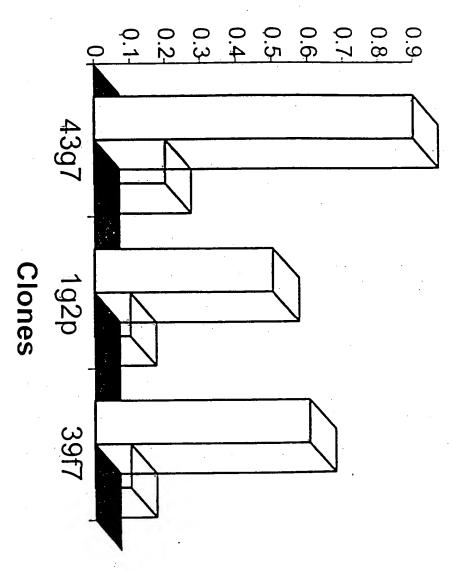
	*			
10 20	) 30		50 60	
1234567890 1234567890	1234567890	1234567890	1234567890 1234567890	
COCKCOCK CLARGEOCK	GATGCAGCTO	GIGCAGICIG	GGGGAGGCTT GGTACAGGCT	<b>:60</b>
0	MOL	V Q S G	GGL VQP	
_				•
CANALITY WITHOUT	CIGRELAGE	CICTUGATICA	CCTTCAGEAG CTAIGCLAIRG	120
G G S L R L S	CAG	SGFT	FSSYAM	•
6 6 5 2 2 -	_	•		
cyclicating consessing	AGGAAAAGG	r creexeress	TATCAGCTAT TGGTACTGGT	180
H W V R Q A P	GKG	LEWV	SAIGTG	•
11 11 0 11 8 11 1	a •••			
CONTROLLAT ACTARCAGE	A CTCCGTGAAG	GCCCGATTCA	CCATCTCCAG AGACAATGCC	240
G G T Y Y A D	s v K	GRFT	I S R D N A	
3 3 1 1 1 3 3				. •
LICELOTOT TOTATOTTO	A AATGAACAG	CTGLGLGCCG	AGGACATGGC TGTGTATTAC	300
KNSLYLQ	M N S	LRAE	D M A V Y Y	
N N D Z I Z E				
TOTAL SALE OF THE SALE ACC	r eccentricies	CITCOCCACO	TCTATTGGGG TCAAGGAACT	360
CARW GHV	G L W	VADV	YWGQGT	
CTGGTCAGG TCTCCTCAG	TGCAGGG	r TCAGGGGGAG	GTGGCTCTGG CGGTGGGGA	420
L V T V S S G	G G G	SGGG	G S G G G	
TOOGREATOC AGRIGACOO	A GICTECATE	C TOCCTGTCTG	CATCIGIAGG AGACAGAGIC	480
S D I O M T O	SPS	SLSA	SVGDRV	
ACCATCACTT GCCGGGGA	TCASSECAT	r agcaattatt	TAGCCTGGTA TCAGCAGAAA	540
TITCRAS	QGI	S N Y L	, AWY QQK	
				•
			CTTTGCAATC AGGGGTGCCA	1600
PGKVPKL	Ł I Y	AAST	LQSGVP	
TCTCGGTTCA GTGGCAGTG	G ATCTCCCAC	A GAITTCACTO	TCACCATCAS CACCCTGCAG	660
SRFS GSG	SGT	DFTI	TISSLQ	
			GIGCCCCTIA CACTITICCC	720
PEDV ATY	Y C Q	K Y N S	APYTFG	
			•	
CAGGGGAGCA AGCTGGAGA	T CAAAGCCCC	c œ		752
OGTKLEI	K			



	14		
10 20	) 30	) 40 50 60	_
1224567890 1234567890	1234567890	1234567890 1234567890 1234567890	
1234367630 1234307030		GIGCAGTCIG GGGGAGGCIT GGIACAGCT	භ
CCARCE CARCE		V Q S G G G L V Q P	
· Q	MQL	V Q S G G G D V Q F	
	•		
GORGOTOCO TGAGACTOTO	CIGIGGAGG	TOTOGRAFICA OCTIVACIAC CTARCOTAIC	120
G G S L R L S	C A G	SGFTFSSYAM	
3			
	י ארכה אם מכני	CIGGAGIGGG TATCAGCIAT TGGIACIGGI	180
CACIGRATIC GUARATIC	, AGGAAAGG	TEWVSATGTG	
H W V R Q A P	GKG	LEWVSAIGTG	
			0.40
GGTGGCACAT ACTATGCAG	A CTCCCTCAAC	COOCEATICA CONTOTONA ACTICADOSO S	240
G G T Y Y A D	s v K	G R F T I S R D N A	
3 9 1 1 1 1 2			
	کا دارد داشاه د	CTGAGAGCG AGGACATGGC TGTGTATTAC	300
AREACHUL IGLARUICE		TRAFFORMA V V V	٠.
K N S L Y L Q	M N S	L R A E D M A V Y Y	
			200
TGTGCAAGAG AGGGGAGCT	r cassaigeact	TOCTTORGG GTCAAGGAAC TOTGGTCACC	360
CAREGEL	GVT	S F W G Q G T L V T	
مستعمستات استعادتها	جندنتالانس د	OTECCTOR COCCUCACATO	420
GICICCICAS GIGGASSICA		G G S G G G S D I	
V S S G G G G	5 6 6		
			480
CAGATGACCC AGTCTCCATC	cieccieic	I GCATCIGIAG GAGACAGAGI CACCATCACT	400
Q M T Q S P S	SLS	ASVG DRV TIT	
TETTERSEE CICLESSEL	TAGCARTER	TTAGOCTOGT ATCAGCAGAA ACCAGGGAAA	540
CRASOGT	s и у	L A W Y Q Q K P G K	
C .			
		C ACTITICCAAT CAGGGGTCCC AFCRGGTTC	600
GITCHARE ICHERCE	المتحاليفات	C ALLINGAAL CASSINCE AICHOSTIC	000
V P K Ł L I Y	AAS	TLQSGVPSRF	
AGIGGCAGIG GATCIGGGA	CASTITICAC C	T CTCACCATCA GCAGGCTGCA GGCTGAAGAT	660
SGSGSGT	DFT	LTIS SLQ PED	
كالتكريكيات عالية المتكادية	בברברבים בב	C ACTOCCCUTT CCACCTICCC CCAACCCACC	720
		SAPW TFG QGT	
VATYYCQ	K I N	SAFWIFG QGI	
			242
AAGGTGGAAA TCAAAGGGG	$\infty$ .		743
K V E I K			•



# A405

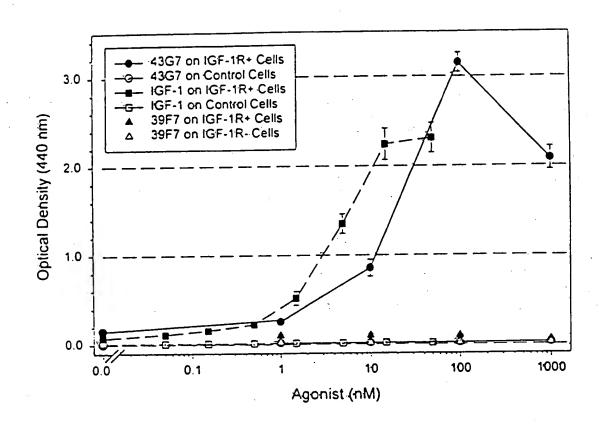


□ BSA

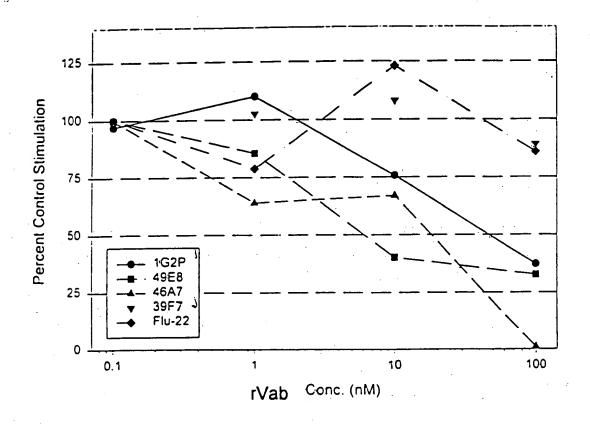
□ IGF-1R

FIGURE 40











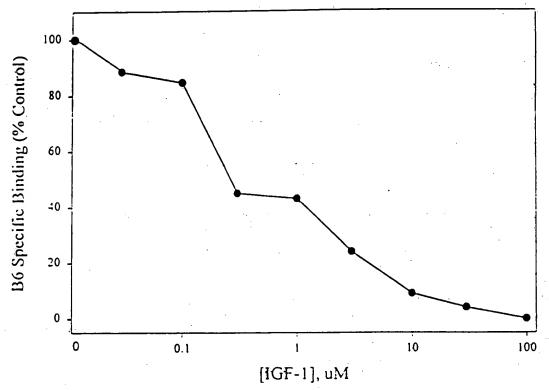


FIGURE 43



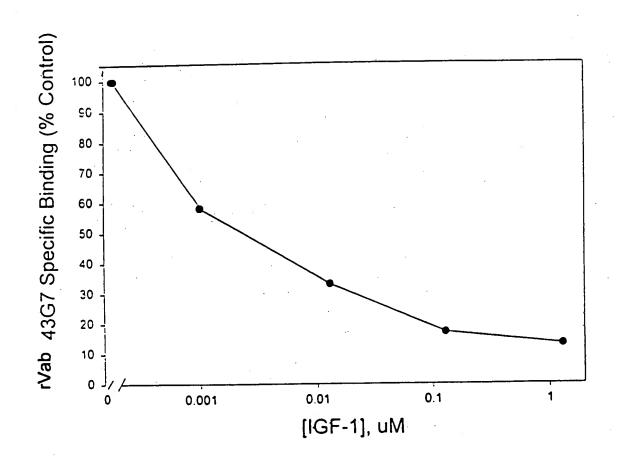


FIGURE 44



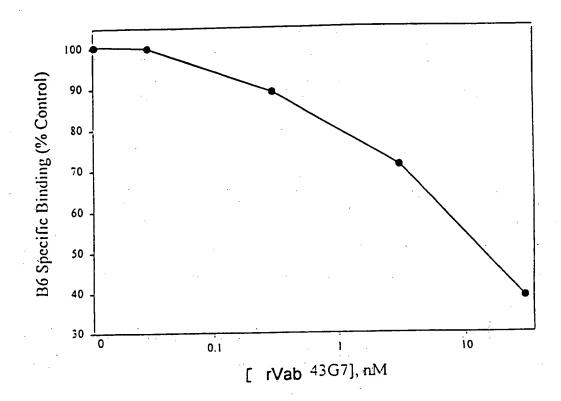
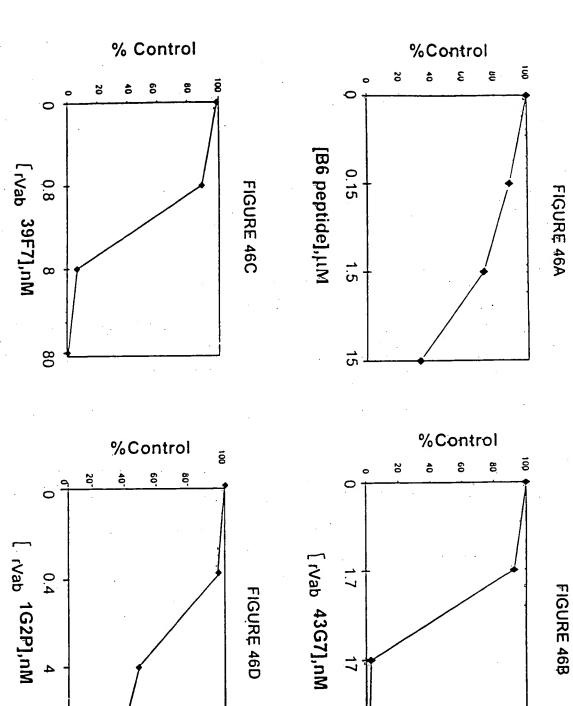


FIGURE 45







F4 E7-2 40G11 40B2 40B12	3011 1131 1131 1131	D10-2	22	CS	Λ8 -	C4	D2	20111 20111	20F1	20D3*	1	
GVGTLTMSSDAFXTWEV  CTESHYVVFQAALDRLEYSWEGS  CETLESHYVVFQAALDRLEYSWES  CHRIMHYVWVQDRDRYINGVRJWYISDRYNPGSAFXRWEID  RMGLQALAHYVKSAGFIFLSSGSVIKGSEGDPFYAWFRLQ	HEAFYDWFSALVDGGYELMG FYGWFSRQLSLTPRDDWGLP	RIGGGWARSEGFYEWFVREL RMFYEWFWSQMGAGPTEGSA	SRDQTNFTFNSAGFYGWFER GAFYRWFHEALVGSERVPDV	LPAGGAQGFAVRGFYEWFRII RDKPTDQEEQNWSFYEWFRII	GHSWALVRHVDRLFYEWFDL	DIGSEGERETAREEM	DPERMQSDVGFYEWFRAAVG WSALLSVMDTGFYAWFDDAV	RVNGNISAPGLVSNKQDGLFYSWFRE VLQNRIIGCDSVSDCFYEWFN	vfwncrsqqldfyewfeqaa RGGGTfyewfesalrkhgag	Group 1: Formula i Would		
1231	LP 1	بر بر	بر بر	<b>-</b>	. р	2 2	ν ω	<b>ب</b> د		18	Found	
+ + + +	+ + +	+ +	÷ +	+ +	÷	+ +	+ + +	+ +	+ +	. +	Ħ	Tar
+ + + + + + + + + + + + + + + + + + + +	‡ ‡ ‡	:	+ + + + + +	· + +	‡	+ + + + + +	+ + + + + + + + + + + + + + + + + + + +	· + + · + + · + +	+ :	÷ ÷	ICF	get

# FIGURE 47



Circuip 2: Formula 6 Motif 2004\*

EIEAEWGPVRCLVYGRCVGG WLDOEWNWVOCEVYGRGCPS

20C11 20A12 Group 3: Formula 2 Motif 201:2 DYKDDRAFYNGLRDLVGAVYGAWD DYKOFYDAIDQLVRGSARAGGTRD

9¢ C6 RGOSDAFYSGLWALIGLSDG DYKORLFYCGIQALGANLGYSGCV DYKDEYSALWGLCGVTGCG

Group 5: Miscellaneous Motif 10

139-3 PEGECCRWWG I PRHWWYRNS WWWGGRNRWWLERWGLGGER

Group 4 and 6: Miscellaneous Motif 10

≥ 22 ≥ 23 LGPLLRWGSEVCGVWPDLCE SMFVAGSDRWPGYGVLADWL VRGFQGGTVWPGYEWLRNAA

GRVALWGPVWPRWWEMSRPV WPGYLFFEEALQDWRGSTED

÷ ÷

FA HILCVLEELEWGASLEGYCSG

BG

ACSSEEVKGPEGELQCLGSI

40D6 FERCRGLETAMOLMBREERDWIIFPHSLEWGAPPPLSG Group 7: Formula 4 Motif

**Group 8: Non-Aligning** Miscellaneous Sequences

FIGURE 48

Found 3 1	Found 1	Found  1  1  1  1	Found 13 3
‡ ‡ ‡ ‡ <del> </del> ₹ ;	- + ‡   ₹ <sub>Ta</sub>	+ + + + + # # Tai	‡ ‡   <b>5</b>
I arget IR IGF  ++ 0 ++ ++ ++ ++	Target   IR   IGF   ++ ++ ++   ++   ++   ++     ++	Target   R   IGF   + + + + + + + + + + + + + + + + + +	, o o o



FIGURE 49A

FIGURE 49B

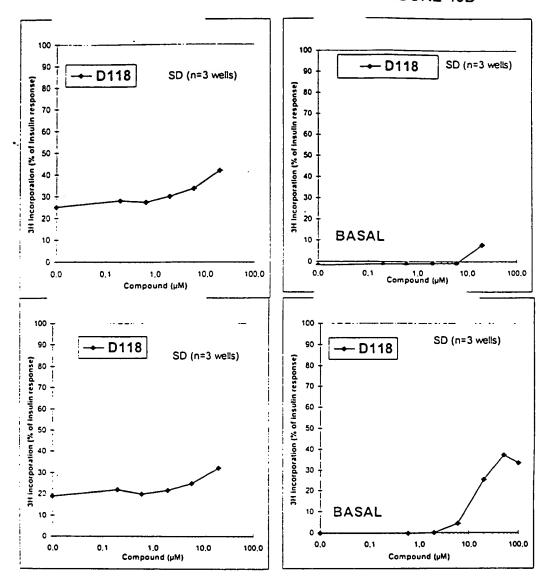
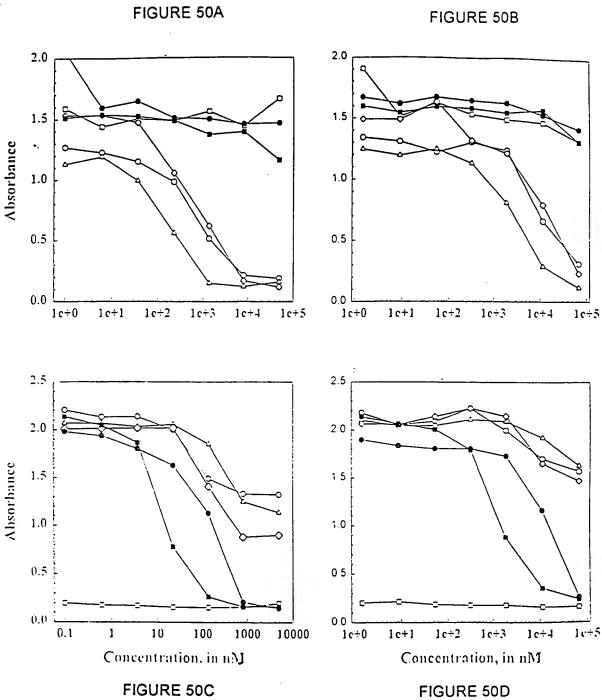


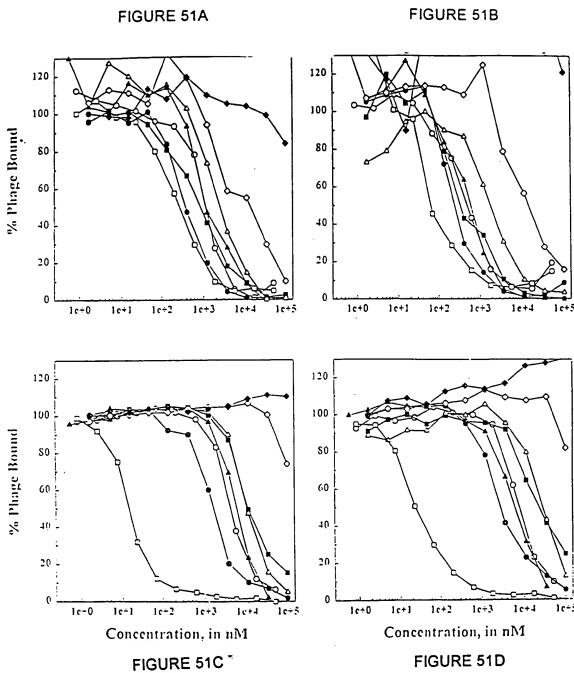
FIGURE 49C

FIGURE 49D











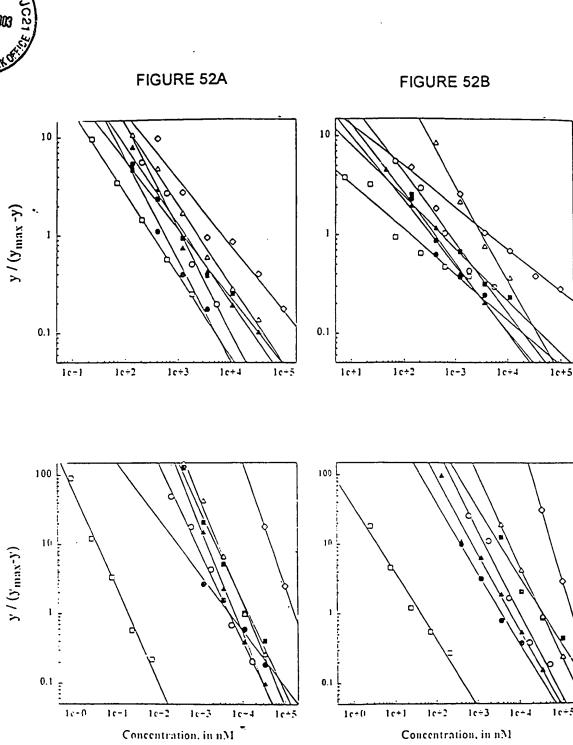


FIGURE 52C

FIGURE 52D



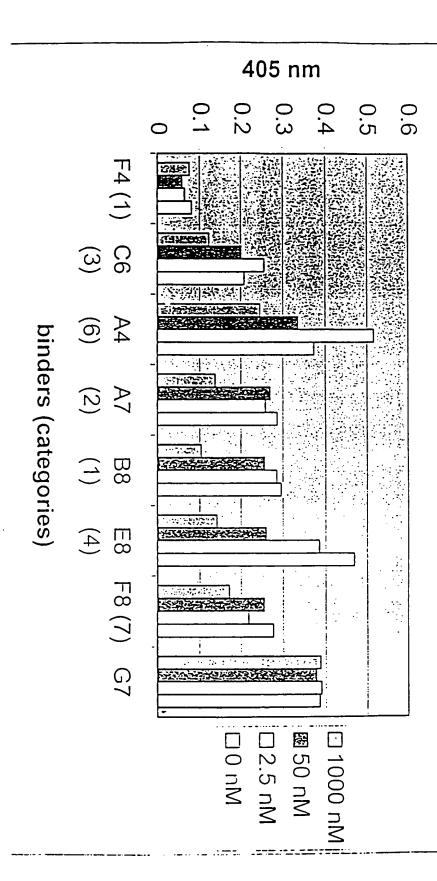


FIGURE 53



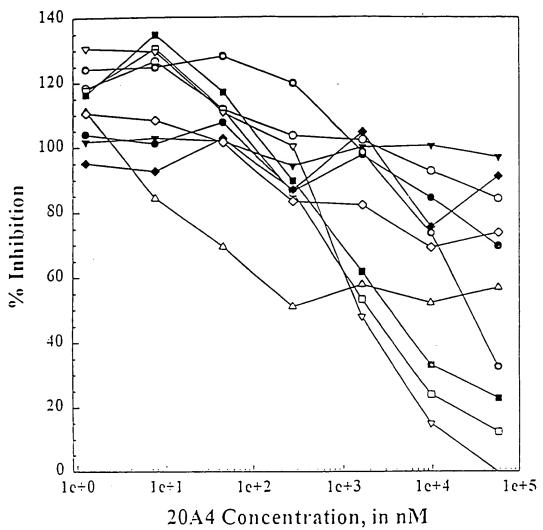


FIGURE 54



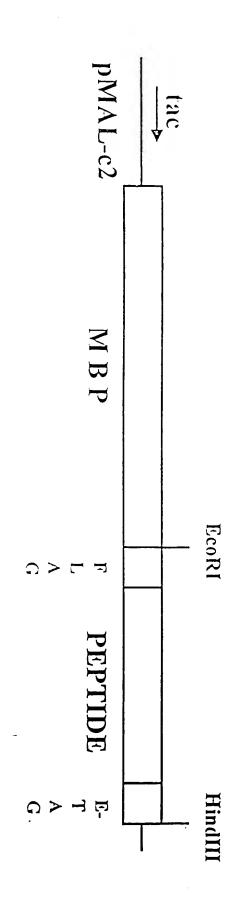
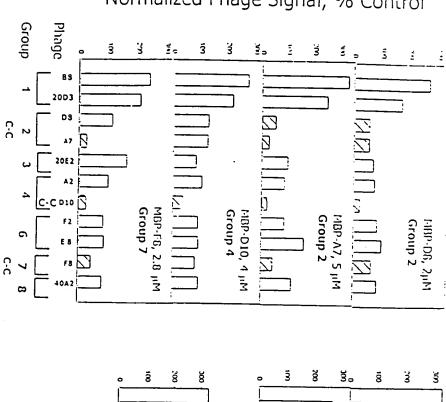


FIGURE 55



# Normalized Phage Signal, % Control



MBP-447, 14 ,IM
FIGURE 56C

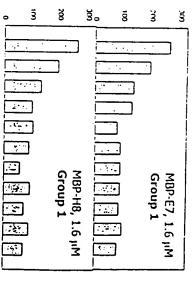


FIGURE 56B

FIGURE 56A



10 20 30 40	
10 20 30 40 50 6 1234567890 1234567890 1234567890 1234567890 1234567890 CCCASCOGG CCATGGGGA CONTRACTOR CONTR	0
CCCASCIGG CCATGGCCGA GGIGCAGCIG GIGGAGCIG GGGAGCCTT GGIAAACCC	0
E V Q L V E S G G G L V K P	
GEGEGICOC TIAGACICIC CIGIGCAGOC TOTOGATICA CITICAGIAA COCCIGGATO G G S L R L S C A A S G F T F S N A W M	
ACCITICACION CONTROLLO ACCUPACIONE TROCCOGNAT TARRACCIANI S $_{\rm c}$ V V R Q A P G K G L E W V G R I K S K	
ACTGATGGTG GGLCANCAGA CTACGCTGCA CCCGTGLARG GCRGATTCRC CATCTCALGL T D G G T T D Y A A P V K G R F T I S R	
CATCATICAA AAAACACCCI GIATCIGCAA ATCAACACC TCAAAACCCA CCACACACCACC D D S K N T L Y L Q M N S L K T E D T A	
GIGTATTACT GTACCACATA CGGGGACGTT TACGACGGG ATTACGATGG GCGCTGGGGT V Y Y C T T Y G D V Y D R D Y D G R W G	
CHARLOTC TOSTCHOOST CTOCTCHAST GRASSCATT CHARCEST TOCTCHAST Q G T L V T V S S G G G G S G G G G S G	
GREGOGRAF COCKCATOCA CATGACOCAG TOTOCATOCT COUTGTOTOC ATCTGTAGRA G G G S D I Q M T Q S P S S L S A S V G	480
GRORGROTICA CORTOROTTO COGGGGGGROTIC CROGGGROTITA GORATTATTI AGCOTOGNAT D R V T I T C R A S Q G I S N Y L A N Y	540
CHARLENARO CHARLANDET TORTAHAGOTO CTGATOTATO CTGALTOCAC TYTGALATOA Q Q N P G N V P N L L I Y A A S T L Q S	600
G333TCCCCAT CTCG37TCAG TG3CAGTGAA TCTGGGAACAG ATTTCAGTCT CACCATCAGC G V P S F F S G S G S G T D F T L T I S	650
ASCOTECHS: CTARRATET TECHNOTIAT TACTETCARA ACTATRACAS TECCOTITIC S L Q P E D V A T Y Y C Q K Y N S A P F	720
ACTUTECORDO CTODIACONA ACTIGINTATO ANALOGOCOG C	761

1	0 20	30	. 40	50	60	
	0 1234567890					
GCCCATCCG	G CCATGGCCGA					60
	E	V Q L	L E S G	GGL	V K P	
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TTAGACTOTO	CIGIGCASCC	TCTGGATTCA	CTTTCAGTAA	CCCCTCCATC	120
G G S	LRLS	CAA	SGFT	F S N	AWM	
AGCTGGGTO	COCERCECTOO	ACCOMMISSES	CTGGLGTGGG	TTGGCCGTAT	TAARACCIAR	180
•	RQAP					
ستتدعيسة	G GGACAACAGA	و کلیک ویل	توتوتييي	CLTCTALLTC V	במבברתרתב	240
	T T D					243
1 2 0		. A A	I V K C		1 5 5	
GLIGHTER	A AAAACACGCT	CIPATOTO	ATC: NO: CO	בררות הב הכוח	٠٠٠	202
	NT L					300
. ב ע ע	1 1	т г О	ra ra 5 L	K I E	D T A	
ب دست دشت م	- CE: CC) C) E:	~~~~	~~~~~		50110011cm	260
	GTACCACATA					360
V 2 E (	TTY	D . W	GVLV	V W G	QGT	
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~						
	TCTCCTC+CC	TGI-GGCGGT	TCLESTEGLE	GIGGCICIGG	CCCLCCCCF	420
T ( T	'SSG	G G G	S G G G	G S G	GGG	
	AGTTGACCCA					480
S D I (	) FIG	S P S	F L S A	S V G	D R V	
						540
T I I (	RAS	S G I	S S Y L	$\forall R, Z$	QQX	
0242634441	TELLATEDOD F	COTGATOTAT	GOTGERTOCA	CTTTGCAAAG	TGGGGTCOCL	600
P G E F	P K L	L I Y	A A S T	L Q S	G /. :	
TCHAGITTC	. GOGGCLETGE	ATCTGGGACA	GATTTCACTC	TCACCATCAG	2429777242	660
S R F S	GSG	SGI	D'F T L	TIS	SLC	
					_	
COTGRADAT	TTGCAACTTA	TTACTGTCAL	CAGCITAATA	GITACCCTTT	CACTITOGGG	720
	A TY					· = <del>-</del>
		<b>.</b>	, <u> </u>		<del>-</del>	
000000000000000000000000000000000000000	. AASTGEATAT	CFFFG./GGG	- د <del>دستان -</del>			753
	. 1. D 1					, ,,,



CLONES VHCDR3 %Inhibition Activity

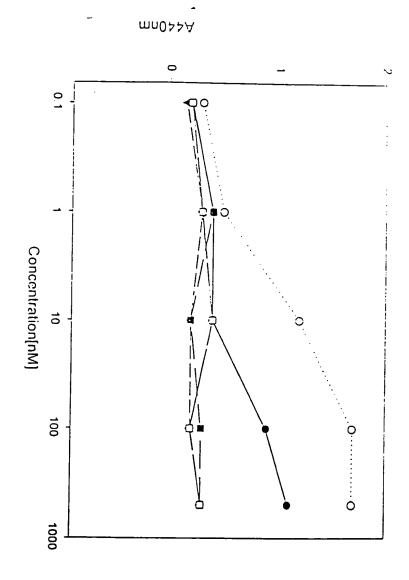
?	118:	PFFV	FY <u>RG</u> QDT	54%
	InsulB: 12H10:	FVNQH <u>LCG</u> SH <u>LVEAL</u> Y L <u>VC</u> C VVYNYA	CGERGFFYTPKT G RG T	42%
Ang?	13-e-4:	VQANDGL	G RES	52%
?	13h9:	GGL	G RRDWL	30%
•	24:	GGRR	H RIG	
?	InsulinA 11a6:	GIVEQCCTSICSLYQ LENYC ENYG		325
::/A		GDØETŰNA		None



FIGURE 60

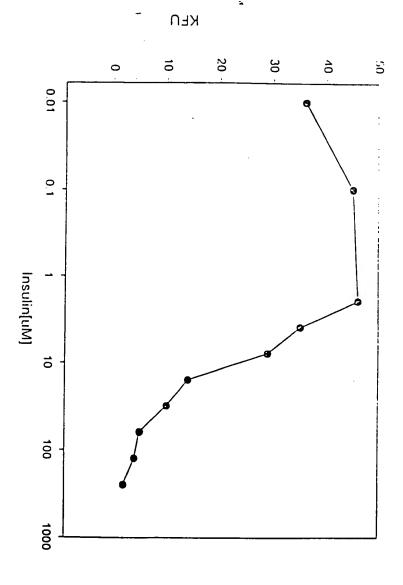
..O.. Insulin in 32D-IL4R-IR-INS-1
——— 13h9 scAb in 32D-IL4R-IR-INS-1
——. 12h10
——— Insluin in 32d-IL4-IR
——. 13h9

-- 12h10 scΛb in 32D-IL4R-IR-INS-1

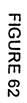


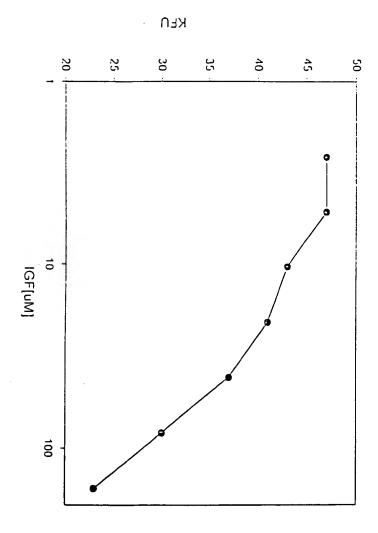














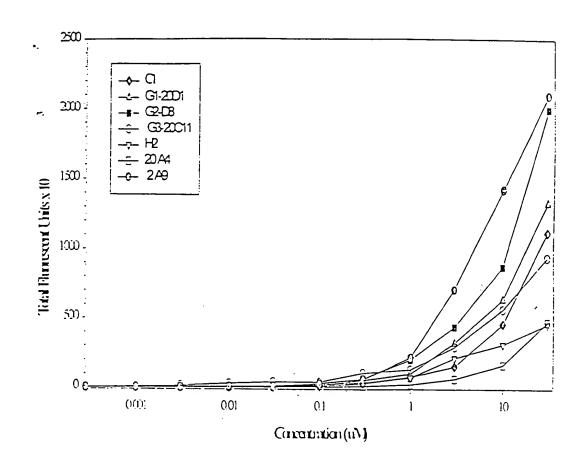


FIGURE 63



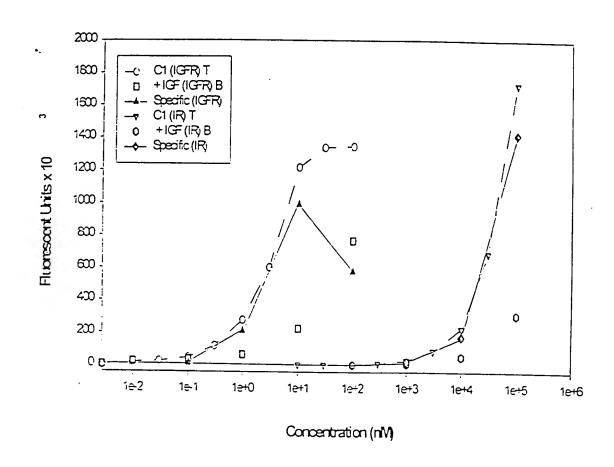


FIGURE 64



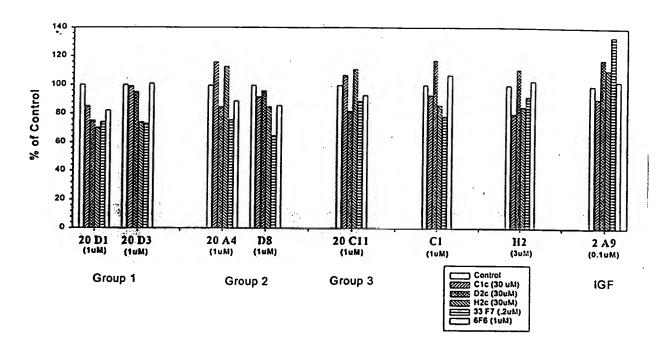


FIGURE 65



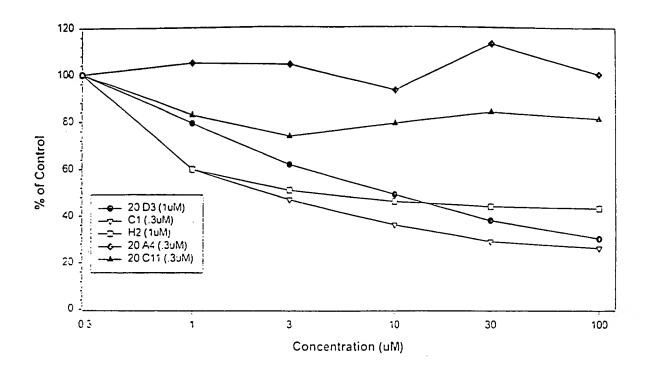


FIGURE 66



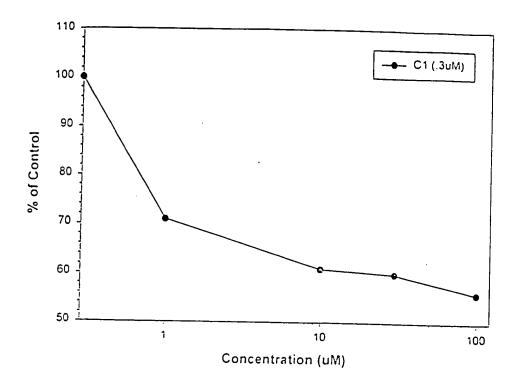


FIGURE 67



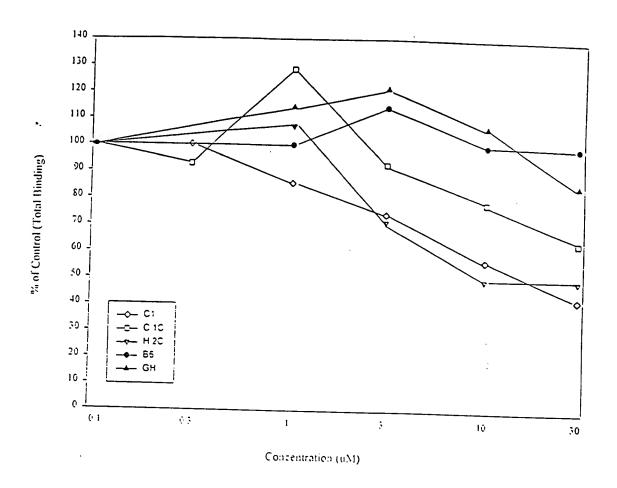


FIGURE 68



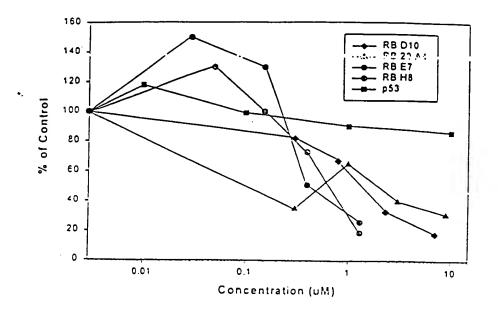
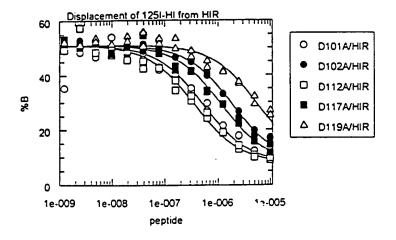
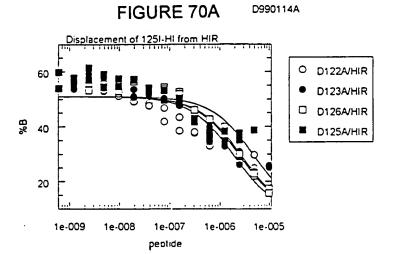


FIGURE 69







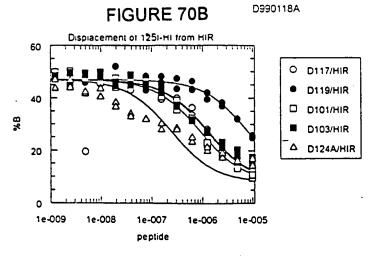
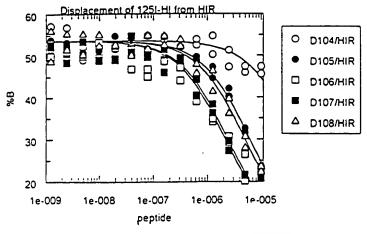
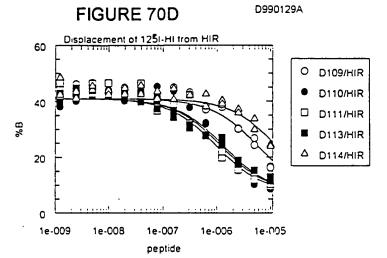


FIGURE 70C

D990126A







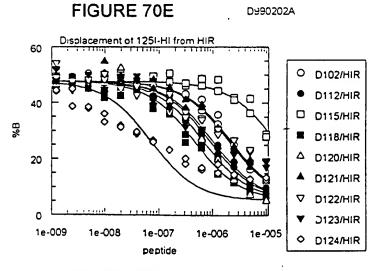
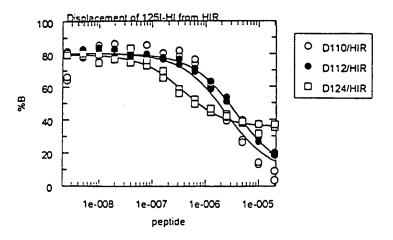


FIGURE 70F

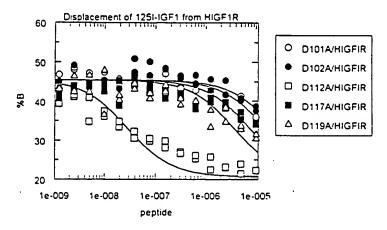
D990205A





## FIGURE 70G

#### D990217A



### FIGURE 70H

#### D990114A

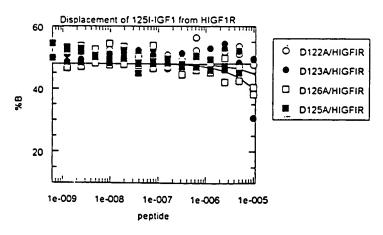
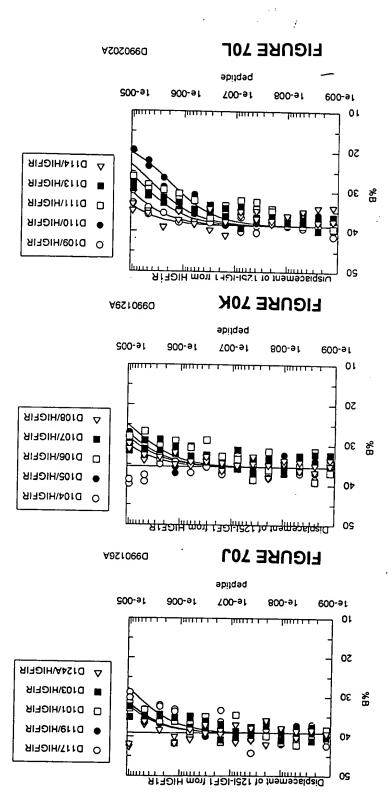


FIGURE 701

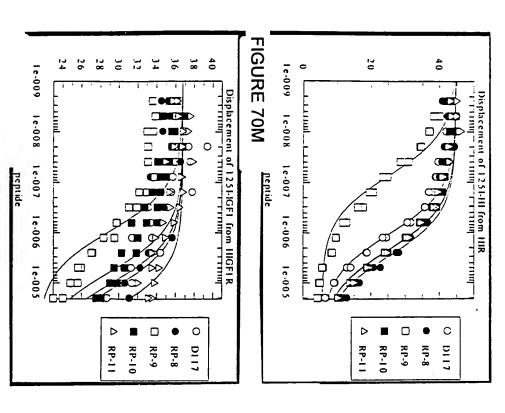
D990118A













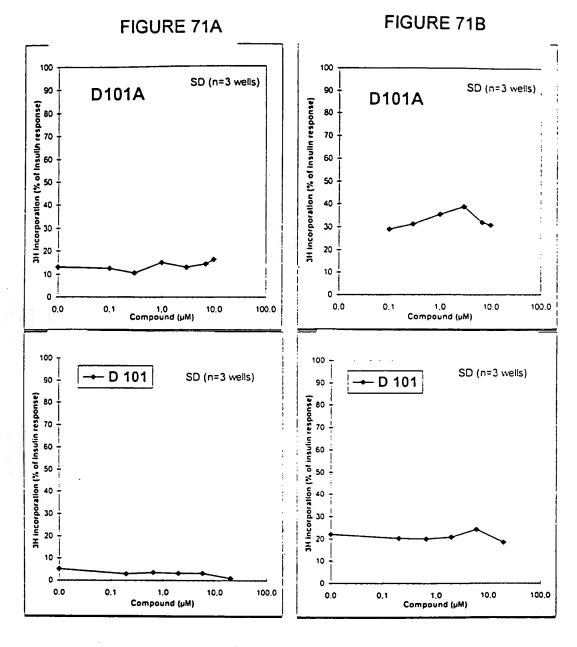


FIGURE 71C

FIGURE 71D



FIGURE 71E

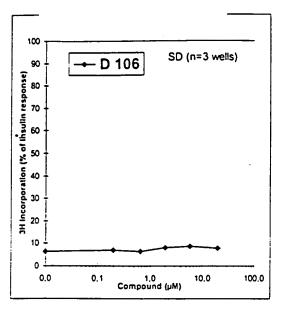
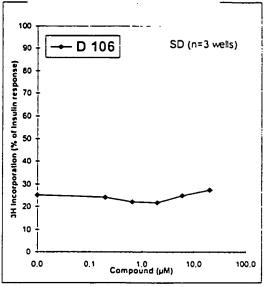
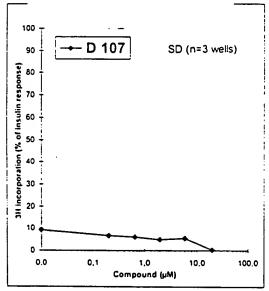


FIGURE 71F





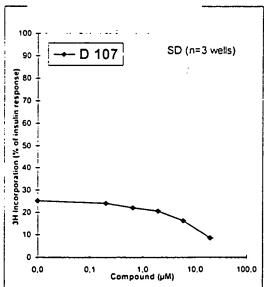


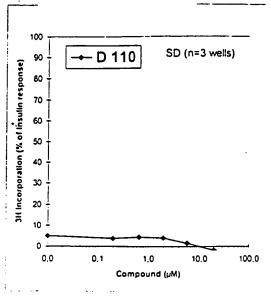
FIGURE 71G

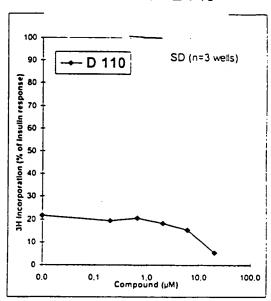
FIGURE 71H

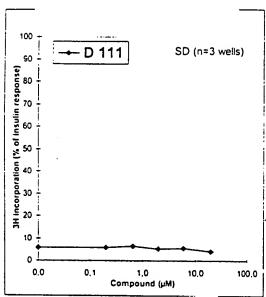


FIGURE 711

FIGURE 71J







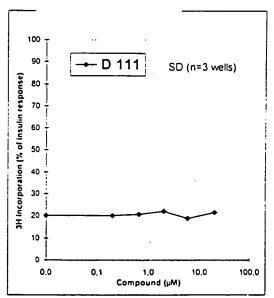


FIGURE 71K

FIGURE 71L





## FIGURE 71N

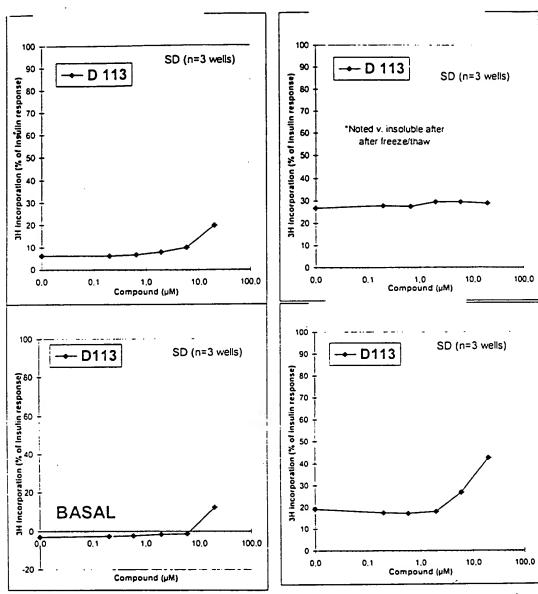


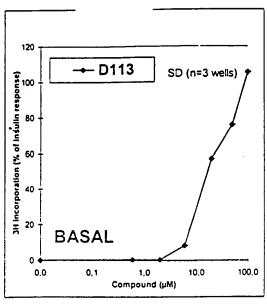
FIGURE 710

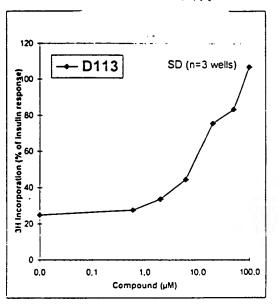
FIGURE 71P

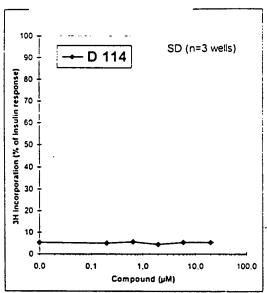


FIGURE 71Q

FIGURE 71R







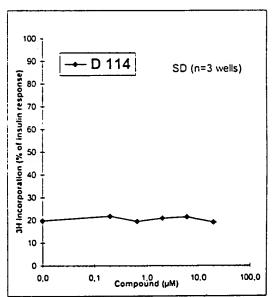


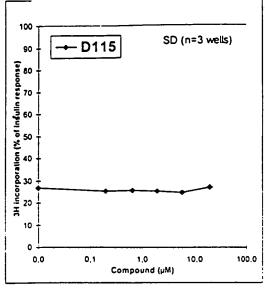
FIGURE 71S

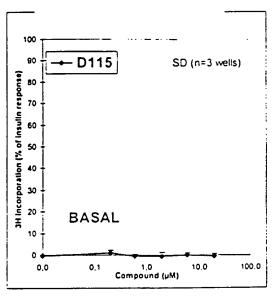
FIGURE 71T

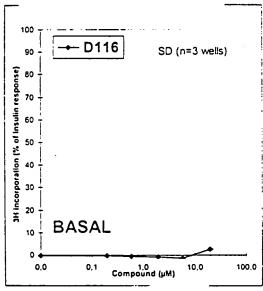


FIGURE 71U

FIGURE 71V







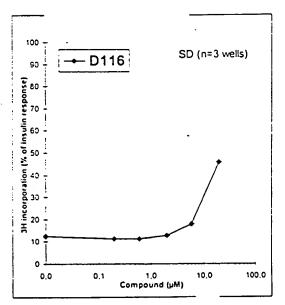


FIGURE 71W

FIGURE 71X



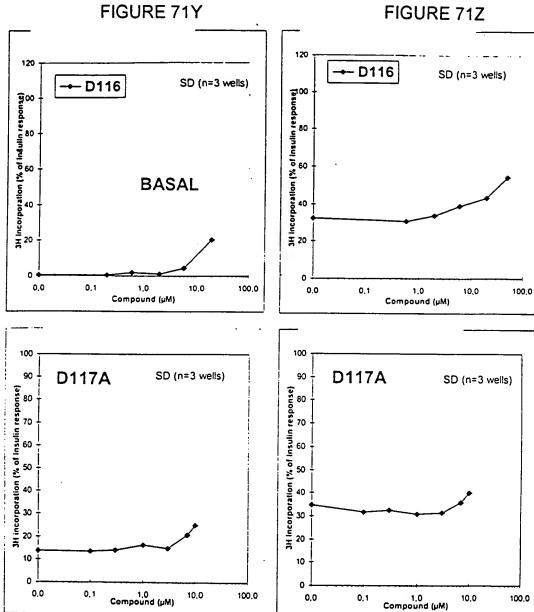


FIGURE 71A2

FIGURE 71B2



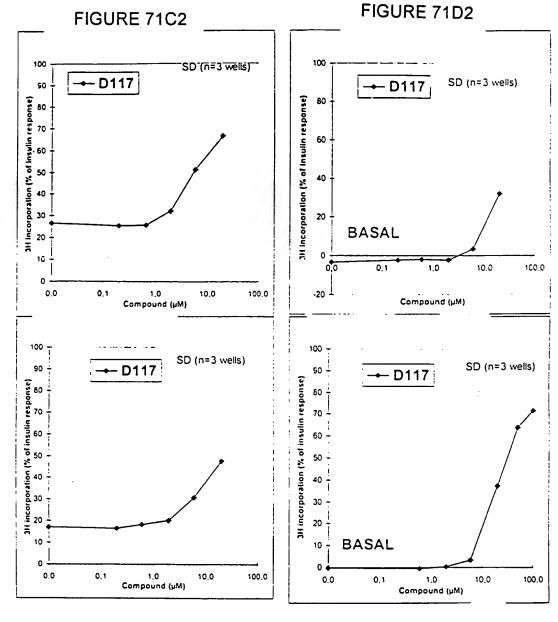
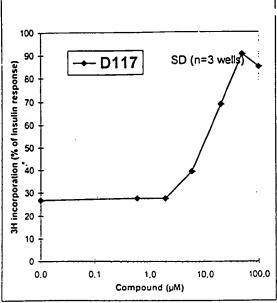


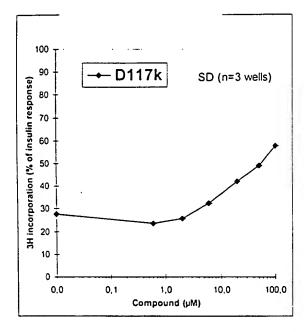
FIGURE 71E2

FIGURE 71F2



FIGURE 71G2





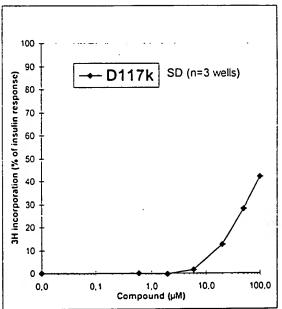
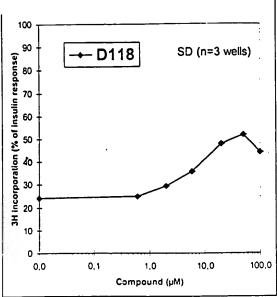


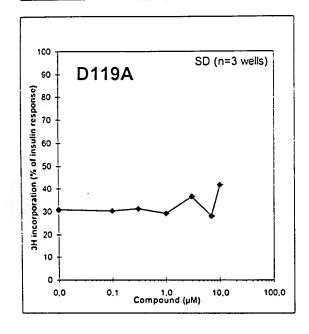
FIGURE 71H2

**FIGURE 7112** 



FIGURE 71J2





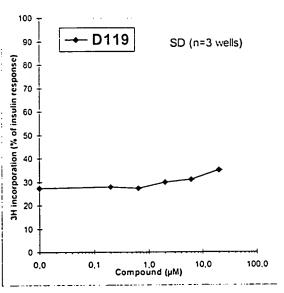
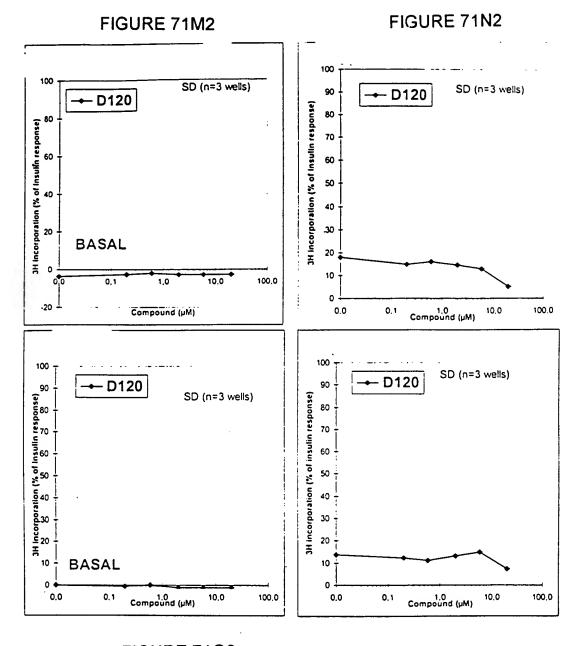


FIGURE 71K2

FIGURE 71L2





**FIGURE 7102** 

FIGURE 71P2



FIGURE 71Q2

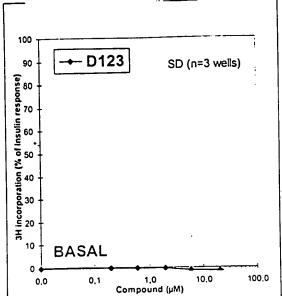
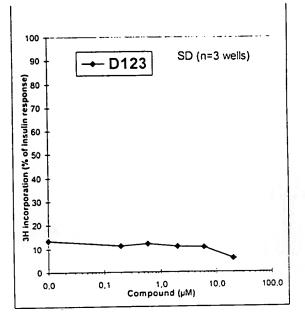


FIGURE 71R2



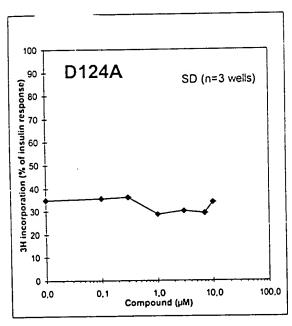


FIGURE 71S2



FIGURE 71T2

FIGURE 71U2

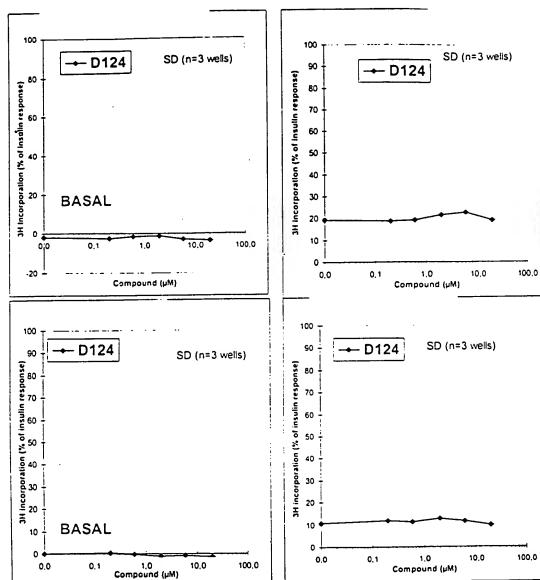
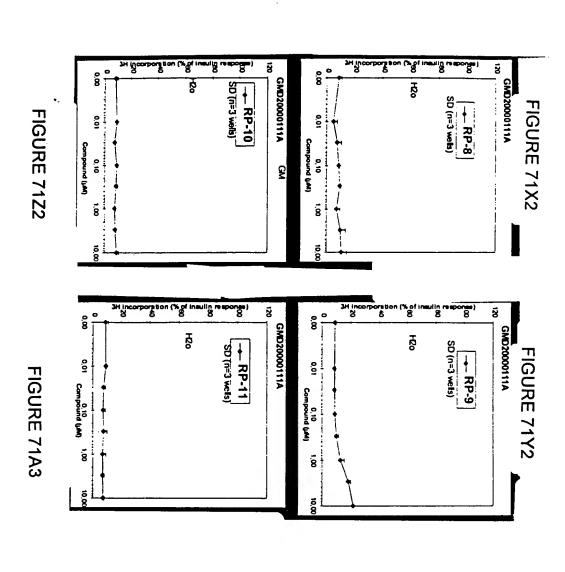


FIGURE 71V2

FIGURE 71W2





S291: Dimer of S204 with linker 9

S204 = Lig-GGGFHENFYDWFVRQVSKK

Linker 9 =

HIR binding =  $1.2*10^{-6}$ 

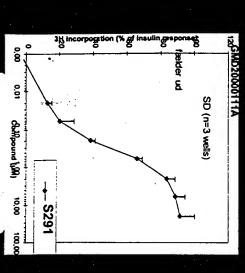
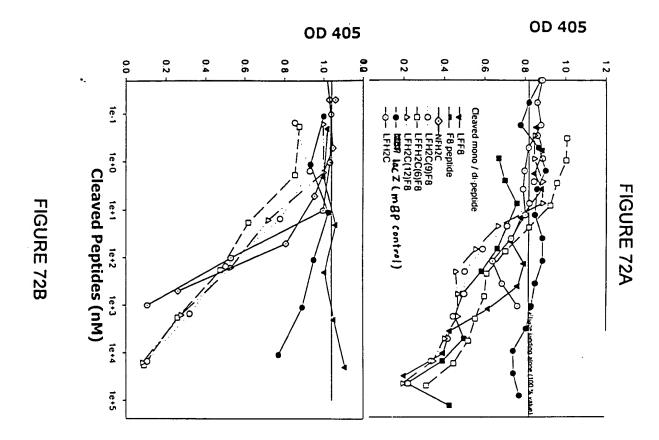


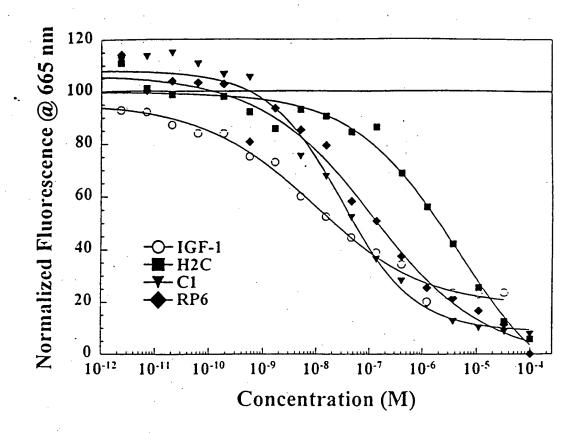
FIGURE 71B3





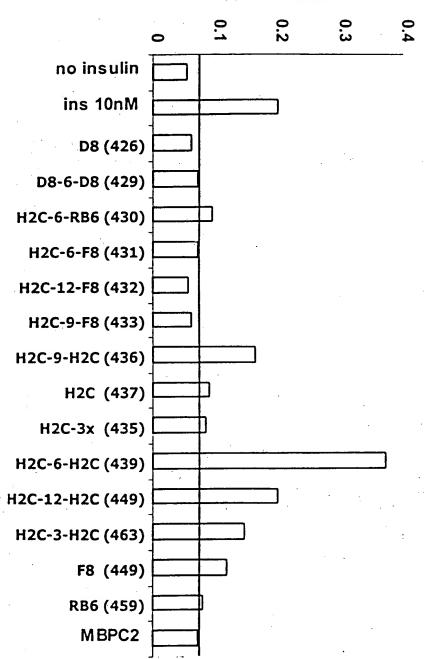












FIGURE